Impact of monocyte differentiation and intracellular infection on processing and presentation of autoantigen

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Abstract

Dendritic cells (DCs) and macrophages are specialized antigen presenting cells that process self and foreign antigens and present them to T cells via major histocompatibility complex molecules, human leukocyte antigens (HLA) in humans, for induction of tolerance or initiation of T cell-mediated immune responses. Related to differentiation state, they have specific phenotypes and functions, and varied interactions with pathogens herein exemplified by *Leishmania donovani* (LD) that parasitize macrophages and propagate within their phagolysosomes. The impact of the differentiation state and intracellular infection on antigen processing and presentation by HLA class I remained undefined. To gain insight, we analyzed and compared the HLA-I self peptidomes of MUTZ3 cell line-derived human immature and mature DCs, and THP1 cell line-derived LD-infected and none-infected macrophages by liquid chromatography-tandem mass spectrometry (LC-MS/MS), as well as proteasome compositions by quantitative RT-PCR, and HLA expression and cell activation states by flow cytometry. We found that the HLA I-presented self-peptidomes of the cells in the different states were heterogeneous and individualized, dominated by nonapeptides with similar HLA binding affinities and anchor residues. They were sampled from source proteins of almost all subcellular locations and from proteins involved in various cellular functions in similar proportion including tumour-associated antigens (TAAs). The persistence of LD within the macrophage, did not affect macrophage activation. However, its impact was observed in self-peptidome heterogeneity, HLA binding affinities, anchor residue preferences, source protein peptide sampling (including TAAs) and HLA and proteasome expression.

Keywords: antigen processing/presentation, dendritic cells, macrophages, *Leishmania donovani,* major histocompatibility complex, mass spectrometry, peptidome

Zusammenfassung

Dendritische Zellen (DCs) und Makrophagen sind spezialisierte antigenpräsentierende Zellen, die eigene und fremde Antigene prozessieren und mittels Haupthistokompatibilitätsmoleküle, humane Leukozytenantige (HLA) im Menschen, T-Zellen präsentieren, um Toleranzen zu induzieren oder T-Zell-vermittelte Immunantworten zu initiieren. Abhängig von ihrer Differenzierung haben sie spezifische Phänotypen und Funktionen undunterschiedliche Interaktionen mit Pathogenen, in dieser Arbeit durch *Leishmania donovani* (LD) repräsentiert, welche in Phagolysosomen der Makrophagen propagieren. Der Einfluss der Differenzierungszustände und von intrazelluläre Infektionen auf die Antigenprozessierung und -präsentation waren weitgehend undefiniert. Um hier Einblick zu gewinnen, haben wir die HLA-I-präsentierten Selbstpeptidome von menschlichen unreifen und reifen DCs, die aus der MUTZ3-Zelllinie generiert wurden, und LD-infizierte bzw. nicht-infizierte aus der THP1-Zelllinie generierte Makrophagen mittels Flüssigchromatographie-Tandem-Massenspektrometrie (LC-MS/MS), sowie die Proteasom-Zusammensetzung per RT-PCR und die HLA-Expression und Aktivierungszustände der Zellen per Durchflusszytometrie analysiert und verglichen. Wir fanden, dass die HLA-I-Selbstpeptidome der Zellen heterogen und individualisiert waren, von Nonapeptiden dominiert wurden und ähnliche HLA-Bindungsaffinitäten und Ankerreste aufwiesen. Sie stammten aus Quellenproteinen aus fast allen subzellulären Lokalisationen und mit unterschiedlichen zellulären Funktionen in ähnlichen Anteilen und schlossen Tumor-assoziierter Antigene (TAAs) ein. Die Persistenz der LD hatte keinen Einfluß auf den Aktivierungszustand der Makrophagen, verursachte aber eine weitgehende Veränderungen des Peptidoms, der HLA-Bindungsaffinitäten und Ankerreste, der Quellproteine einschließlich TAAs und der HLA- und Proteasom-Expression.

Stichwörter: Antigenprozessierung / -präsentation, dendritische Zellen, Makrophagen, *Leishmania donovani*, Haupthistokompatibilitätskomplex, Massenspektrometrie, Peptidom

Abbreviation

ANN	Artificial neural networks
APC	Antigen presenting cell
CD 34+	Pluripotent stem cells
CD	Cluster of differentiation
CD4+	Cluster of differentiation 4
CD8+	Cluster of differentiation 8
CHAPS	3-[(3-cholamidopropyl) dimethylammonio]-1-propanesulfonate
CID	Collision-induced dissociation
CTLs	Cytotoxic T cells
DC	Dendritic cells
ECD	Electron-capture dissociation
ELISpot	Enzyme-linked immunosorbent spot
ER	Endoplasmic reticulum
ERAAP	Endoplasmic reticulum amino peptidase associated with antigen processing
ESI	Electrospray ionization
ETD	Electron-transfer dissociation
GM-CSF	Granulocyte-macrophage colony stimulating factor
HLA	Human leukocyte antigen
HPLC	High performance liquid chromatography
hTERT	Human telomerase reverse transcriptase
IEDB	Immune epitope database
IL-4	Interleukin-4
KDa	Kilo dalton
LARP1	La-related protein 1
LC- MS/MS	liquid chromatography tandem mass spectrometry

LD	*Leishmania donovani*
LMP2	Proteasome subunit beta type-9
LMP7	Proteasome subunit beta type-8
M/z	Mass to charge ratio
MBOA7	Lysophospholipid acytransferase 7
MECL1	Proteasome subunit beta type-10
MHC	Major histocompatibility complex
MS	Mass spectrometry
MS/MS	Tandem mass spectrometry
MUTZ3	Cytokine-dependent CD34+ human acute myeloid leukaemia cell line
MUTZ3 iDC	MUTZ3 derived immature dendritic cells
MUTZ3 mDC	MUTZ3 derived mature dendritic cells
PDB	Protein database
PI	Propidium iodide
PININ	140 kDa nuclear and cell adhesion-related phosphoprotein
PRAME	Preferentially expressed antigen in melanoma
PSME3	Proteasome activator complex subunit 3
RHAMM	Receptor for hyaluronic acid–mediated motility
ROS1	Proto-oncogene tyrosine-protein kinase ROS
RPMI	Roswell park memorial institute medium
TAAs	Tumour associated antigens
TAP	Transporter associated with antigen processing
TBS	Tris-buffered saline
TFA	Trifluoroacetic acid
THP1	Human monocytic cell line derived from an acute monocytic leukemia patient
THP1MΦ	THP1 derived macrophages

THP1MΦi	THP1 derived macrophages infected with *Leishmania donovani*
THP1MΦiy	THP1 derived macrophages infected with YFP transfected *Leishmania donovani*
TRRAP	Transformation/transcription domain-associated protein
UHRF1	E3 ubiquitin-protein ligase UHRF1
URP2	Femitin family homolog 3
WT1	Wilms tumor protein
YFP	Yellow fluorescent protein

Amino acids one and three letter code

Ala A Alanine	Gly G Glycine	Pro P Proline
Arg R Arginine	His H Histidine	Ser S Serine
Asn N Asparagine	Ile I Isoleucine	Thr T Threonine
Asp D Aspatic acid	Leu L Leucine	Trp W Tryptophan
Cys C Cysteine	Lys K Lysine	Tyr Y Tyrosine
Gln Q Glutamine	Met M Methionine	Val V Valine
Glu E Glutamic acid	Phe F Phenylalanine	

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1. Introduction

I.1 The immune system

The immune system is a collection of cells, tissues and molecules within organisms that defends against invading pathogens and cancer; and consists of two arms; the innate and the adaptive immune system. The innate immune response is the first line of defense and entails; Firstly, tight junctioned epithelial cells which line the internal and external body parts such as the skin, gastrointestinal, urogenitol and respiratory tract creating a physical barrier between the internal milieu and the pathogen-containing external milieu. Secondly, mucus secretion by internal mucosa epithelia, that coat pathogens and inhibit their attachment. Thirdly, movement by epithelia cilia in respiratory tract that expulse pathogen. Fourthly, microbicidal secretions by epithelial cells such as gastric acid in the gastrointestinal tract, phospholipase A and lysozyme in tears and saliva, and beta-defensins in genitourinary tract (1,2). In addition, in case a pathogen bypasses the epithelial barrier, phagocytes are chemotactically recruited at the infection site, where they recognize, engulf and destroy invading pathogens (3-5). Two types of circulating phagocytes are recruited at the infection site; the neutrophils which are short lived and then the monocytes which differentiate into long lived tissue-resident macrophages or dendritic cells. Neutrophils and macrophages express pathogen recognition receptors (PRRs) that recognize pathogens, infected cells, damaged cells or cancer cells via pathogen associated molecular patterns (PAMPs) and damage-associated molecular patterns (DAMPs). The binding of PRRs to PAMPs or DAMPs triggers transcription of pro-inflammatory cytokines, chemokines, type I interferons, antimicrobial proteins and phagocytosis (6). The neutrophils and macrophages phagocytose the pathogen, infected cell, damaged cell or cancer cells into phagosome which fuse with lysosomes to form phagolysosome. The phagocytosed contents are destroyed by enzymes such as proteases, glycosidases, and sulfatases, and leukocyte-derived toxic products such as nitric oxide, superoxide anion and hydrogen peroxide which are released in a process termed respiratory burst. While neutrophils die shortly after phagocytosis, macrophages persist

and serve as antigen-presenting cells activating the adaptive immune response also known as antigen-specific immune response (7,8). Immature DCs have a comparable gene expression profile with macrophages, but with a lower endo-phagocytic capacity and major histocompatibility complex (MHC) class II expression. (9-12). They can capture both self and foreign antigen in diverse tissues, migrate to secondary lymphoid organs, and present processed antigens via MHC molecules to T lymphocyte cells, linking the innate and adaptive immune response (13) (see **Figure 1**). In adaptive immune response, more so the cell mediated, tissue-resident immature DCs take up antigen in an inflammatory context generated by cell damage, inflammatory cytokines or microbial components and undergo a maturation process to mature DCs. The maturation process is accompanied by epithelia adhesion reduction, endo-phagocytic down regulation, costimulatory molecules (CD40, CD80 and CD86) and MHC molecules upregulation (14,15). The mature DCs migrate into draining lymph nodes or the spleen, and prime antigen-specific T-cell responses (13,16,17). Once activated, cytotoxic T cells (CTLs) also known as CD8+ T cells recognize their targets i.e. the infected cells and tumuor cells by binding to antigen-derived peptide associated with MHC class I molecule (discussed later). Upon binding the targets cells, the CD8+ T cells destroy them by releasing membrane pore-forming proteins such as perforin and proteolytic enzymes such as granzyme (18-20). By contrast CD4+ T cells activated by binding antigen-derived peptide associated with MHC class II molecule assist other white blood cells in immunologic processes, including maturation of B cells into memory B cells and plasma cells, and activation of macrophages and cytotoxic T cells (20,21).

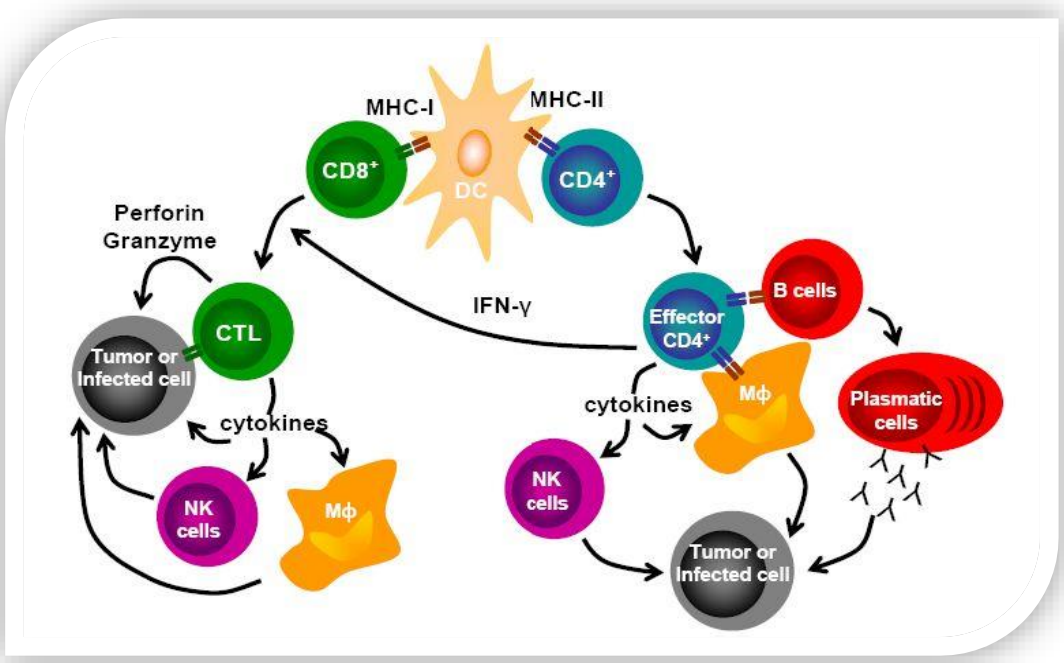


Figure 1. The central role of DCs and T cells in the adaptive immune response (from (21))

I.2 The major histocompatibility complex

The major histocompatibility complex (MHC) or human leukocyte antigens (HLA) complex in human is a gene complex located within chromosome 6 and contains more than 220 genes of diverse functions including those encoding proteins of immune system. The genes in this complex are divided into basic groups including; class I and class II. The MHC class I genes consists of HLA-A, HLA-B, and HLA-C while the MHC class II genes consists of HLA-DR, HLA-DQ and HLA-DP. The MHC I and MHC II differ in both the structure and cell type they are expressed.

The MHC I is expressed on all nucleated cells, and is a heterodimer consisting of two polypeptide chains; α chain that consists of α1, α2, and α3 domains, and the light chain (β2-microglobulin). The α chain and β2-microglobulin are linked together through the noncovalent interaction of β2-microglobulin and α3 domain, while the domains α1 and α2 form the peptide

binding groove which is closed on both sides allowing 8-12 amino acids peptides to bind the molecule as illustrated in **Figure 2**. The α1, α2 and α3 subunits are encoded by three different genes HLA-A, HLA-B and HLA-C which are mostly heterozygous and highly polymorphic resulting to high diversity of HLA class I molecules. Currently, there are 3,968 HLA-A, 4,828 HLA-B and 3,579 HLA-C alleles (http://hla.alleles.org). This diversity impacts on the nature and composition of the peptide-binding groove, and hence the peptide repertoire presented on the surface by MHC class I molecules, for CD8+ T lymphocytes.

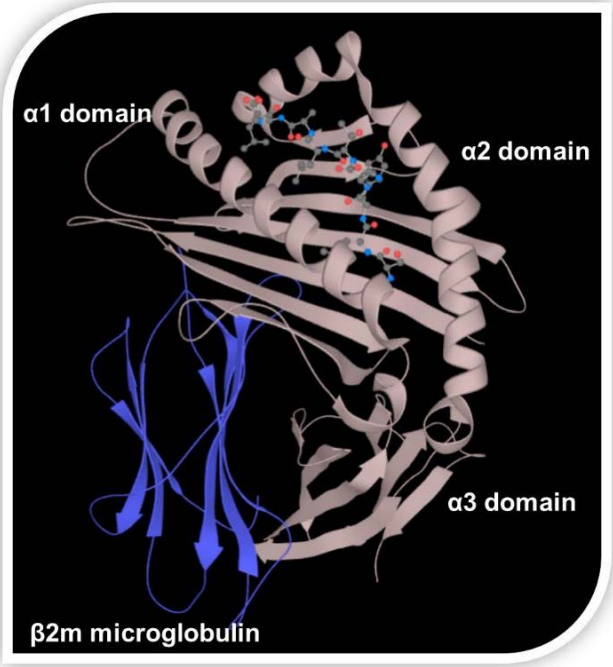


Figure 2. Crystal structure of the human HLA-A*02:01complex as a flat-ribbon model. The α-subunit is coloured brown and the β2m is coloured blue. The human immunodeficiency virus p17 Gag-derived peptide SLYNTVATL located in the binding groove of the HLA-A*02:01 molecule is shown as red and blue balls, and sticks. The PDB file 1t20 (22) was used for the visualization and representation of the crystal structure was performed with Litemol 3D molecular viewer software (San Diego, USA).

MHC Class II molecules are expressed in all cell types, especially professional antigen-presenting cells (APCs) such as macrophages, B cells, and dendritic cells (DCs). MHC class II

consists of α chain (α1 and α2 domain) and β chain (β1 and β2 domain) which are anchored to cell membrane via transmembrane domains. The peptide-binding groove formed by α1 and β1 domains is open on both ends, allowing binding of longer peptides (13-17 amino acids). MHC class II molecules are also highly polymorphic resulting to high diversity. To date, 2376 HLA-DRB1, 1,142 HLA-DQB1 and 894 HLA-DPB1 alleles have been identified (http://hla.alleles.org), that differ in the structures of their peptide binding grooves, which inturn impact the specificity of peptide bound on MHC class II molecules, for CD4+ T lymphocytes.

I.3 Peptide binding to MHC class I molecules

MHC class I molecules bind peptides with high promiscuity, and 10,000 different peptides can be bound by an MHC class I allomorph species (23-28). The MHC-bound peptides stabilise the MHC molecule, without which it is unstable (29). The peptides bind to the MHC molecules via the interaction of the peptide N-terminal amino and C-terminal carboxy group with the conserved amino acids at the ends of peptide binding groove, via hydrogen bonds (30).The vast majority of MHC I peptides are 8-12 amino acids long, but longer peptides can be accommodated by the bulging of the peptide at the central portion (31-33). Though the MHC class I molecules bind many different peptides, only a subset of all the available can bind to each allele (31,34). The MHC I binding groove consist of six binding pockets, designated by the letters A to F (35), as illustrated in **Figure 3**. Due to HLA polymorphism these binding pockets vary greatly in size or physicochemical properties allowing the binding of only those peptides with amino acids that are complementary to the structure and chemical properties of the binding pockets of particular HLA (36,37). For example, in HLA-A*02:01 molecule pockets there a preference of isoleucine, leucine or methionine at position 2 (P2) and a preference for large hydrophobic side chains at the carboxy terminus of the peptide (PW) (38). The amino acids at P2 and carboxy terminus of the peptide are termed dominant anchor motifs, while the rest are termed secondary anchor motifs. The dominant anchor motifs confer

significant binding energy, but the total binding energy to the MHC is the sum contribution of all the residues in the binding cleft (39).

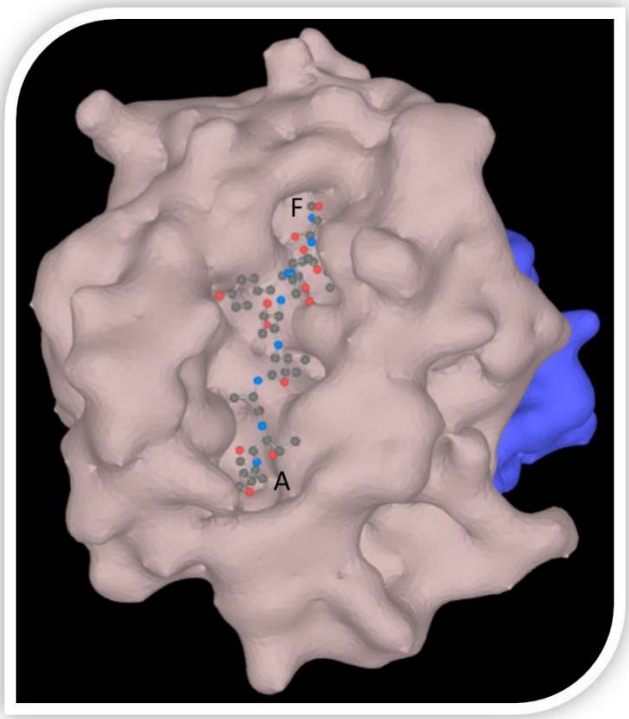


Figure 3. Surface of the HLA-A*02:01 molecule binding groove. The binding pockets A to F and the bound human immunodeficiency virus p17 Gag-derived peptide SLYNTVATL are shown. The PDB file 1t20 (22) was used for the mapping and representation of HLA-A*02:01 binding groove was carried out using LiteMol 3D molecular viewer software (San Diego, USA).

I.4 Antigen processing and presentation

The antigen processing and presentation represent a multi-step process by which an antigen either intracellular or extracellular is processed and presented at the surface of an antigen presenting cells to be exposed to the surveillance of CD4+ and/or CD8+ T cells **(see Figure 4)**. The antigen processing involves two distinct pathway each dedicated to the presentation of antigens by MHC class I molecules or MHC class II molecules.

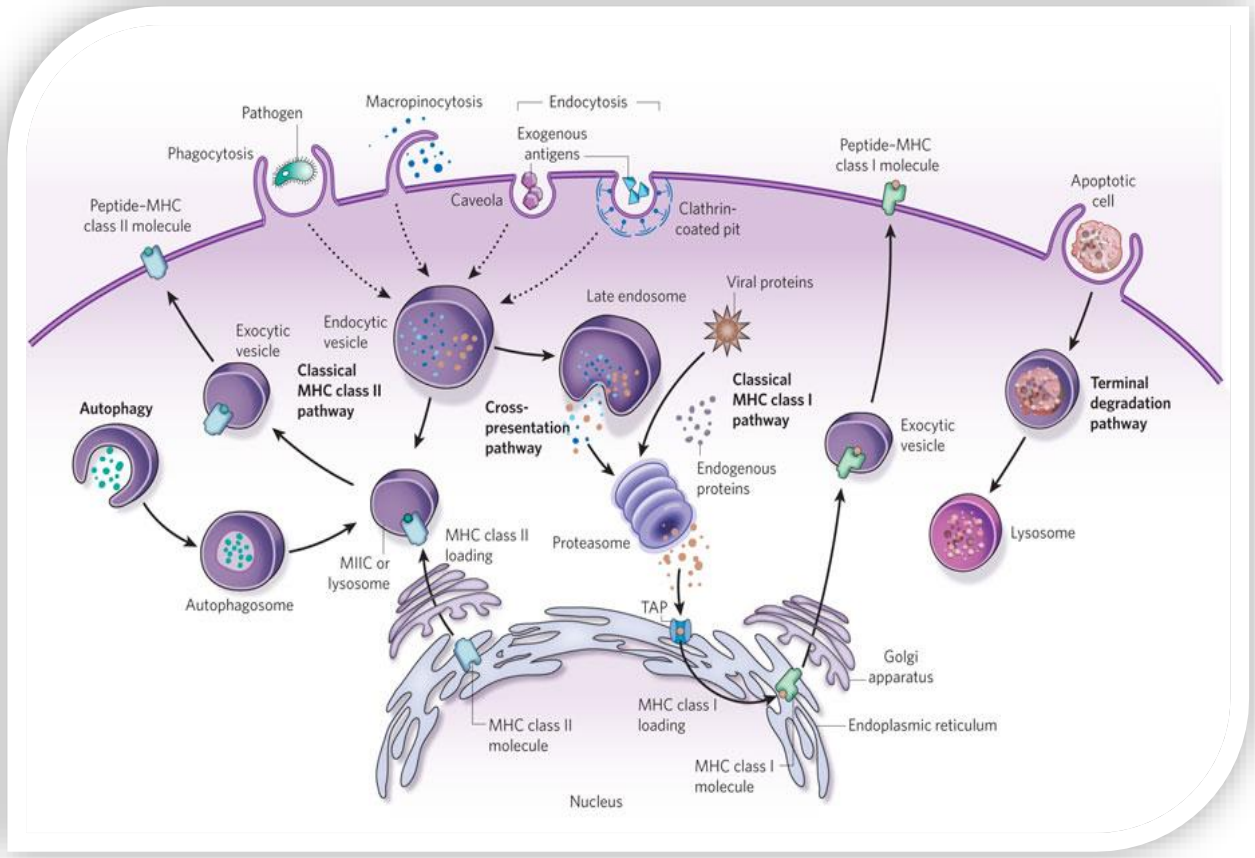


Figure 4. Representation of MHC Class I and MHC Class II antigen processing pathways and cross presentation (from (40))

In the MHC Class I pathway, an antigen is loaded onto MHC class I molecules through a so called classical pathway, where endogenously expressed self or viral proteins in the cytosol are processed through a multicatalytic protease complex, the proteasome (constitutive and immunoproteasome) (41,42). The constitutive proteasome consists of the 20S core and two regulatory 19S subunits. The 20S core a 28-subunit barrel-like particle has three catalytically active subunits β1, β2 and β5, which hydrolyse the peptide bond (43-46). The β1, β2 and β5 subunits exhibit caspase-like, trypsin-like, and chymotrypsin-like activities; which hydrolyse after acidic, basic and hydrophobic amino acids residues, respectively (47-49). The activity of the proteasome can be altered by stimulation of the cells with inflammatory cytokines such as interferon-gamma (INF-γ) replacing the active β1, β2 and β5 subunits with their homologues (immunoproteasome); β1i (LMP2), β2i (MECL1) and β5i (LMP7), that exhibit chymotrypsin-

like, trypsin-like and chymotrypsin-like activities, respectively. This altered cleavage pattern by the immunoproteasome enhance the quantity and quality of the generated peptides for presentation on MHC class I molecules (50-55). The degraded products by the proteasome vary in length (2-25 amino acids) (51). In vitro studies show that more than 70% of all proteasome-generated peptides are too short to bind to MHC molecules, and only 15% has the correct length for MHC binding (56) .Others are extended at the N-terminus and are further degraded by aminopeptidases such as tripeptidyl peptidase II (TPPII) localised in the cytosol, with a preference for peptides longer than 15 amino acids (57). After processing in the cytosol, the peptides are transported into the endoplasmic reticulum (ER) via transporter-associated with antigen processing (TAP) where peptides longer than 10 amino acids are rapidly degraded by aminopeptidases such as endoplasmic reticulum amino peptidase associated with antigen processing (ERAAP) (58). The kinetics of the degradation of shorter peptides in ER proceeds much slower, as substrate detection is dependent on the sequence length (59). In the absence of the ERAAP, longer peptides are presented by MHC molecules, but such MHC-peptide complexes are unstable (60). The assembly of MHC-I heavy chain- β_2m heterodimers with the peptides is coordinated by the peptide loading complex, which is composed of a disulphide-linked dimer of tapasin and thiol oxidoreductase ERp57, calreticulin and TAP molecules (60). The MHC I peptide complex is then transported to the cell surface via the Golgi apparatus for presentation to CD8+ T cells (61).

Extracellular antigens can also be presented by MHC class I molecules via an antigen processing pathway called cross-presentation (42). In this pathway, exogenous antigens that have been endocytosed are cross-presented on MHC class I molecules. The antigen is either loaded in endocytic compartments or escapes the endosomes into the cytosol, where it undergoes processing via the proteasome similarly to classical MHC I antigen processing and presentation pathway.

In MHC Class II pathway, exogenous particles, proteins or pathogens are taken into the cell through various pathways, including phagocytosis. These exogenous antigens are then processed in endocytic vesicles and subsequently loaded onto MHC class II molecules that have been assembled in the ER. Prior to peptide loading, the MHC class II αβ-chain dimers are assembled as a nonameric complex with the invariant chain (Ii) that protect against premature peptide or protein interactions in pre-lysosomal compartments. This complex traffics to the lysosome MHC class II compartment (MIIC), where Ii is subjected to sequential proteolysis. The final cleavage product, a peptide known as class II-associated Ii peptide (CLIP) occupying the peptide-binding groove and is realized during peptide loading via an exchange reaction catalyzed by the chaperone-like molecule HLA-DM (62). The peptide (~10–16 amino acids) – MHC class II complexes are then moved through exocytic or recycling vesicles to the surface of the cell and presented to CD4+ T cells (62).

The collection of peptides presented by the MHC molecules at the cell surface is termed the HLA-peptidome. The HLA-peptidome has been shown to be influenced by the expression and rate of degradation of the source proteins, efficiency of peptide loading onto MHC molecules, the binding affinities of the individual peptides to the presenting MHC molecules (63-65), and the decay kinetics of specific MHC peptide complexes (66).

I.5 *Leishmania*, infection and cell mediated immune response

Leishmania are obligate intracellular protozoan parasites in vertebrates, of the order Kinetoplastida and the family Trypanosomatidae transmitted by the bites of infected female phlebotomine sandflies (67). *Leishmania* are causative agent of a spectrum of diseases collectively termed leishmaniasis endemic in 98 countries in Africa, Asia, South and Central America and Southern Europe. With 12 million people currently infected, and approximately 2 million new cases and 20 and 50 thousand deaths occurring yearly (68,69). Leishmaniasis is

a neglected tropical disease (https://www.cdc.gov), with no vaccine, and whose treatment includes the use of only 4 toxic compounds; sodium stibogluconate, miltefosine, Paromomycin and lipid formulations of amphotericin B. The disease is caused by about 21 of 30 *Leishmania* species, which include; *L. donovani* complex consisting of *L. donovani* and *L. infantum* (also known as *L. chagasi* in the New World), *L. mexicana* complex consisting of *L. mexicana, L. venezuelensis and L. amazonensis; L. tropica, L. aethiopica and L. major*, and the subgenus Viannia consisting of L. *braziliensis, L. guyanensis, L. panamensis* and *L. peruviana*. The different species are morphologically indistinguishable and only differentiable by molecular methods and monoclonal antibodies (https://www.cdc.gov). Depending on virulence of the infecting *Leishmania* species, geographic region and the host immune response leishmaniasis can have different clinical manifestation in human **(Table I)**. The main clinical forms of the disease include; visceral leishmaniasis (VL) a systemic disease characterised by fever weight loss, enlargement of the spleen and liver, and anaemia; cutaneous leishmaniasis (CL) characterised by one or several ulcer(s) or nodule(s) in the skin; mucocutaneous leishmaniasis (MCL) characterised by progressive destructive ulcerations of the mucosa, extending from the nose and mouth to the pharynx and larynx (70). Other forms include; diffuse cutaneous leishmaniasis (DCL) characteristised by numerous nonulcerating nodules with an abundant parasite load in the skin (71) and post kala-azar dermal leishmaniasis (PKDL) characterised by a macular, maculo-papular or nodular rash on the skin and is a complication of VL, frequently observed after treatment (72).

Table I. *Leishmania* species, geographic distributions and different clinical manifestation in human

Parasite	Clinical forms[a]	Geographic distributions
L. donovani	(A)VL, PKDL	China
	AVL, PKDL	India, Nepal, Bangladesh
	CL	Sri Lanka
	ZVL, AVL, PKDL, CL	East Africa, Sudan, Ethiopia
L. infantum	ZVL, ZCL	Southern Europe
		Eastern Mediterranean
		China
L. chagasi	ZVL, ZCL	Central and South America
L. major	ZCL	Middle East,
		Southwest Asia
		Africa
L. tropica	ACL, ZCL, LR	Middle East, Southwest Asia
		Africa
L. aethiopica	CL, (MCL), DCL	East Africa
L. mexicana	ZCL, DCL	Central America
L. amazonensis	ZCL, DCL	Central and South America
L.braziliensis	CL, MCL	Central and South America
L. panamensis	CL	Central and South America
L. guyanensis	CL	Central and South America

[a]AVL: anthroponotic visceral leishmaniasis; ACL: anthroponotric cutaneous leishmaniasis; DCL: diffuse cutaneous leishmaniasis; LR: leishmaniasis recidivans; MCL: mucocutaneous leishmaniasis; PKDL: post kala-azar dermal leishmaniasis; ZCL: zoonotic cutaneous leishmaniasis; ZVL: zoonotic visceral leishmaniasis (Adapted from (73)).

In its life cycle **(see Figure 5)**, *Leishmania* exist in a dimorphic state; the flagellated, motile promastigote form (15-30 μm in length and 5 μm in breadth) found in the midgut of sandfly vectors and the non-motile amastigote form (3–6 μm in length and 1–3 μm in breadth) found within phagolysosome of the vertebrate host macrophages, and devoid of external flagellum. The life cycle begins when metacyclic promastigotes are inoculated into the host by infected female sandfly during blood meal. The promastigotes are then taken up by neutrophils and macrophages, but since neutrophils are short lived, they only serve as serve as intermediate host cells, while macrophages which are phagocytes as well as antigen presenting cells are the final host cells (74-76). The

promastigotes are internalized into macrophage phagolysosomes where they transform into none motile amastigotes. The amastigotes are able to survive the harsh milieu in the phagolysosome, multiply, and eventually rapture the macrophages and infect new macrophages (77). The amastigotes are then taken up by female sandfly during a blood meal from a *Leishmania* infected person. Within a period of 4 to 25 days, the amastigotes transform to promastigotes and multiply in the midgut gut of the infected sandfly, and are inoculated in a new host during another blood meal, thus completing the cycle (78).

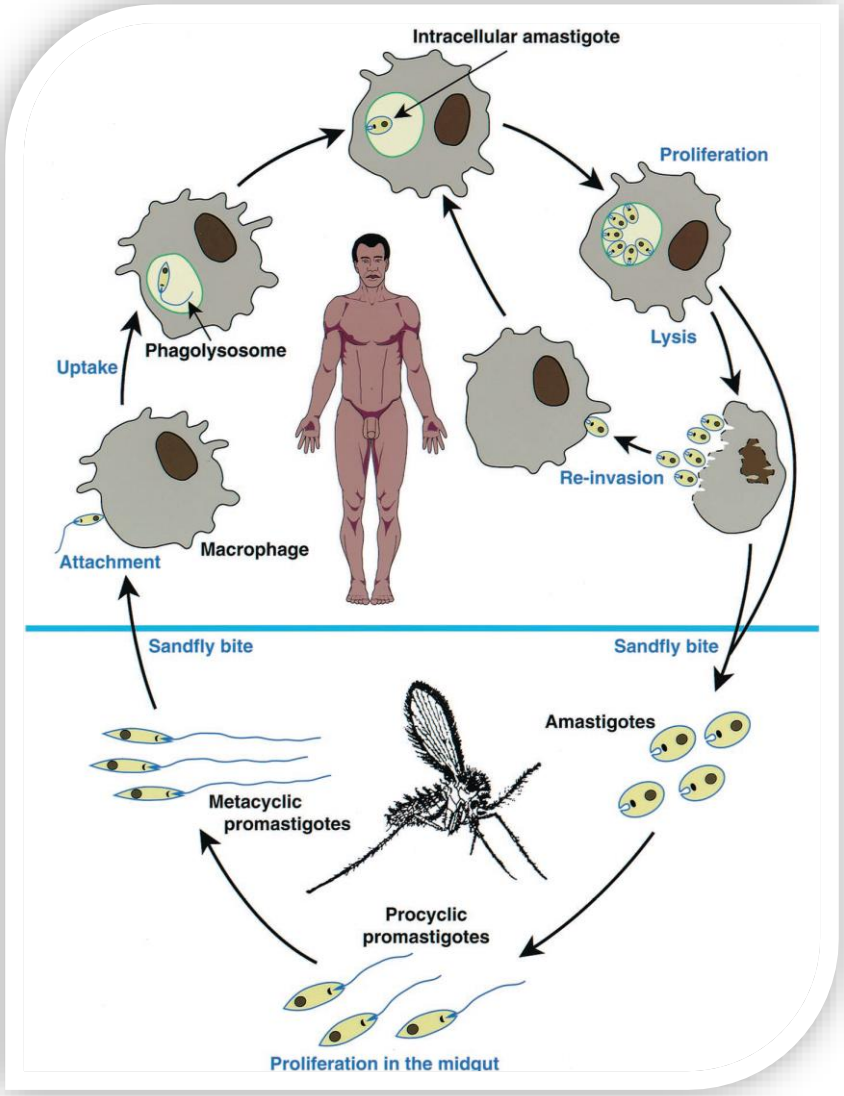


Figure 5. Representation of the *Leishmania* life cycle (Source (73))

Leishmania are able survive and multiply in the harsh milleu in macrophage phagolysosome through subversion of the host immune system and promotion of pro-parasitic host factors (79). The infection of macrophages by *Leishmania* leads to production of immuno-regulatory cytokines such as IL-10 and TGF-β that are known to inhibit/deactivate macrophage functions (80-82). *Leishmania* also encode arginase augmenting host cellular arginase activities thus inhibiting the production of inducible nitric oxide synthase (iNOS), an enzyme which catalyzes L-arginine to generate nitric oxide (NO) (83). NO is a toxic molecule that plays a major role in killing intracellular parasites (84,85). *Leishmania* also avoid exposure to oxidants, by subverting the free oxygen species (ROS) within the phagolysosome through diverse mechanisms including heme degradation and prevention of the NADPH oxidase complex assembly by inhibiting phosphorylation of cytosolic p47phox; a key event for the NADPH oxidase activation (86,87). The *Leishmania* infection has also been shown to down modulate MHC molecules expression on macrophages (88,89), but impact of *Leishamania* infection on antigen processing and presentation in macrophages, which are the primary hosts, remain undefined.

I.6 Dendritic cells and macrophage cell models

Cytokine-dependent CD34+ human acute myeloid leukemia cell line (MUTZ3) derived DCs are similar to human DCs in many respects such as; a similar expression profile both in the immature and the mature forms (90,91), antigen processing and presentation, and ability to induce specific T-cell proliferation (92). Human monocytic leukemia cell line THP1 derived macrophages (THP1MΦ), on the other hand, are similar to native monocyte-derived macrophages in several aspects including differentiation and phagocytosis (93-96).

The MUTZ3-derived DCs and THP1-derived macrophages (THP1MΦ), have been extensively used as models for studying human dendritic cells and macrophages immune functions and responses towards intracellular pathogens (12,15,96-98), and given their transient proliferative

ability of CD34+ derived precursors, they constitute an unlimited supply of human dendritic and macrophage cells. MUTZ3-derived DCs and THP1MΦ represents suitable *in vitro* cell line model systems to study and compare the HLA peptidomes of DCs at different states and macrophages to gain insights into how different differentiations impact antigen processing and presentation, and how *Leishmania (L. donovani)* influences antigen processing and presentation in human macrophages.

I.7 Peptidomics in antigen processing and presentation

Peptidomics represent a novel approach to analyze naturally occurring peptides/epitopes associated to MHC molecules **(see figure 6)**. When supported by specialized proteomics tools, peptidomics approaches are now allowing in-depth elucidation of the HLA-peptidome. Analysis of these peptides is of pivotal importance in fundamental studies of antigen processing and presentation, and identification of T cell epitopes for vaccine design.

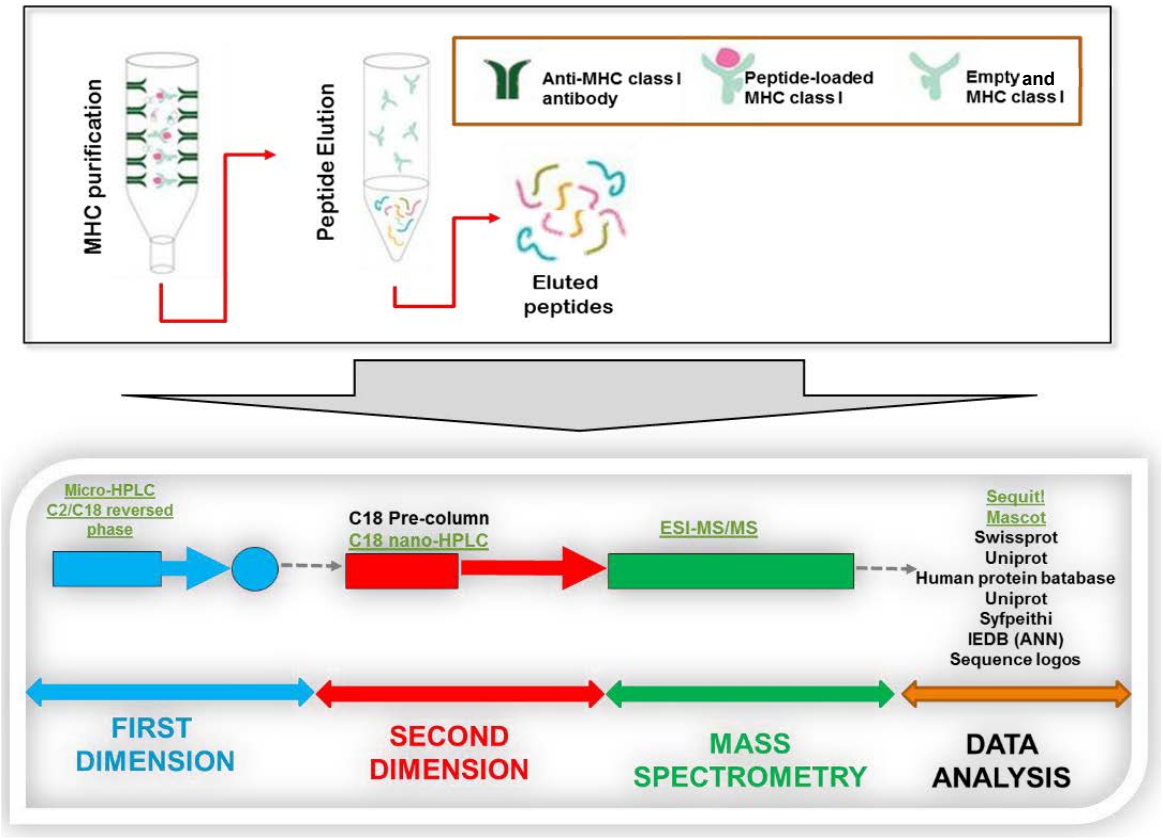


Figure 6: Representation of HLA-peptidome analysis process

In that regards, the high-performance liquid chromatography-electrospray ionization- tandem massspectrometry (HPLC–ESI–MS/MS), which is the current state of the art technology that allows fast identification of several hundreds of MHC ligands in one experimental approach, is used (23,99). In this setup, a complex peptide sample is first separated by HPLC using a reverse phase column that separates peptides by their hydrophobicity. The eluted peptides are then directly subjected to soft ionization by an online coupled electrospray ionisation (ESI) device followed by fragmentation in a collision chamber by low energy collision induced dissociation (CID). In CID, one peptide species out of a mixture is selected in the first mass spectrometer and is then dissociated by collision with an inert gas, such as argon or helium. The resulting fragments are separated in the second part of the tandem mass spectrometer, producing the tandem mass spectrum, or MS/MS spectrum. Several bonds along the peptide backbone are fragmented forming ions types b and the y ions, which denote fragmentation at the amide bond with charge retention on the N or C terminus, respectively (see **Figure 7**). Ion types c and z at the N terminus and C terminus may also be obtained by fragmenting the peptide backbone by electron-capture (ECD) and electron-transfer dissociation (ETD) were peptide ions undergo non-ergodic fragmentation upon incorporating of a thermalised electron, either directly (ECD) or via transfer from an electron-donor anion (ETD)(100-102).

The obtained experimental fragmentation spectra is then matched against a calculated spectrum for all peptides in the protein databases using a number of different algorithms such as MASCOT(103), SEQUEST(104), X! TANDEM (105), MAXQUANT or OMSSA (106). Peptides can also be sequenced denovo (i.e. sequencing without assistance of a linear sequence database) using sequit software (107), allowing for identification of mutations and peptides not listed in databases.

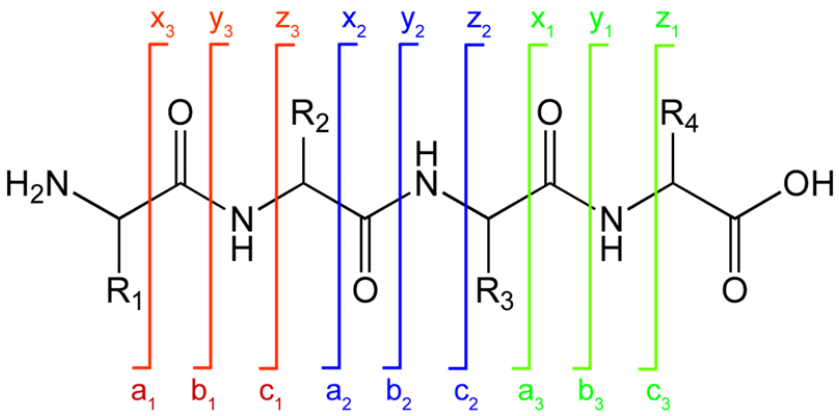


Figure 7. Nomenclature for the product ions generated in the fragmentation of peptide molecules by tandem mass spectrometry as per Roepstorff and Fohlman (108). Peptide fragment ions are indicated by a, b, or c if the charge is retained on the N-terminus and by x, y or z if the charge is maintained on the C-terminus. The subscript indicates the number of amino acid residues in the fragment. R1, R2, R3 represent the side chains of the amino acid residues. In collision induced dissociation (CID) ion type's b and y are formed.

I.8 Aim of Study

Dendritic cells (DCs) and macrophages are specialized antigen presenting cells that process self and foreign antigens and present them to T cells via major histocompatibility complex molecules, human leukocyte antigens (HLA) in humans, for induction of tolerance or initiation of T cell-mediated immune responses. Related to differentiation state, they have specific phenotypes and functions, and varied interactions with pathogens herein exemplified by *Leishmania donovani* (LD) that parasitize macrophages and propagate within their phagolysosomes. The impact of the differentiation state and intracellular infection on antigen processing and presentation by HLA class I remained undefined. The objective of this study is to gain insight on this, through the analysis and comparison of HLA-I self peptidomes of MUTZ3 cell line-derived human immature and mature DCs, and THP1 cell line-derived LD-infected and none-infected macrophages by liquid chromatography-tandem mass spectrometry (LC-MS/MS). Focusing on;

- Number of shared HLA-I peptides and source proteins,
- Peptide lengths, HLA allele specificity and binding affinities
- Frequency of anchor motifs on dominant anchor positions on MHC
- Subcellular locations and molecular functions of source proteins
- MHC-presented leukemia TAAs peptides

In addition, through the analysis and comparison of proteasome compositions by quantitative RT PCR and HLA expression and macrophage activation by flow cytometry methods.

2. Materials and Methods

2.1 Cell lines

The commercially acquired human myeloid leukemia-derived cell line MUTZ3 (DMSZ GmbH, Braunschweig, Germany) heterozygous for HLA-A*02:01, HLA-A3, HLA-B44 and HLA-B56 (92,109,110) was grown in α-MEM medium (Gibco, Grand Island, NY, USA), supplemented with 10% conditioned medium from bladder carcinoma cell line 5637, 20% heat-inactivated fetal calf serum (FCS) (Biochrom, Berlin, Germany), 100 µg/ml streptomycin-penicillin (Gibco, Grand Island, NY, USA) and 50 µM β-mercaptoethanol (Sigma, Steinheim, Germany) at 37°C under 8% CO_2.

The acute monocytic leukemia-derived human cell line THP1 (ATCC TIB-202) homozygous for HLA-A*02:01, HLA-B*15:11 and HLA-C*03:03 (111) was grown in RPMI 1640 medium (Invitrogen, Karlsruhe, Germany) supplemented with 10% heat-inactivated FCS (Biochrom, Berlin, Germany) and 100 µg/ml streptomycin-penicillin (Gibco, Grand Island, NY, USA) at 37°C under 8% CO2.

The HeLa cell line (ATCC CCL-2) was cultured in Iscoves Basal medium (Biochrom, Berlin, Germany) supplemented with 10% heat-inactivated FCS (Biochrom, Berlin, Germany) at 37°C in a humidified atmosphere with 8% CO2. The HeLa cell line clone 33/2 (HeLa A2+/IP) that stably expresses the three inducible proteasome subunits LMP2, MECL1 and LMP7 (112); kindly provided by Prof. P. M. Kloetzel, Charité, Berlin, Germany) were cultured in the same conditions and medium with 2 µg/ml puromycin (Roche, Mannheim, Germany) and 300 µg/ml hygromycin (Roche, Mannheim, Germany).

The T2 cells from Prof. Peter Cresswell (Yale, New Haven, CT, USA) were cultured in DMEM (Gibco-BRL, Karlsruhe, Germany) with 10% heat-inactivated FCS (Biochrom, Berlin, Germany) at 37°C in 8% CO2.

2.2 Parasites

The wild type LD MHOM/IN/02/BHU5 (BHU5) (113) promastigotes were established from splenic aspirates of an Indian patient and cultured in M199 culture medium (Gibco, Grand Island, NY, USA) supplemented with 20% heat-inactivated FCS (Biochrom, Berlin, Germany) at 25°C. The YFP-transfected LD (YFP-BHU5) promastigotes were cultured in the dark in the same medium with 50 µg/ml hygromycin (Roche, Mannheim, Germany).

2.3 Generation of immature and mature DC, and macrophages

To generate the MUTZ3 iDCs, MUTZ3 cells were differentiated for 7 days in the presence 20 ng/mL recombinant human IL-4 (Pep Rotech, Rock hill, NJ, USA), 100 ng/ml recombinant human GM-CSF (Genzyme, Cambridge, MA, USA), and 2.5 ng/mL recombinant human TNFα (Strathmann Biotech, Hamburg, Germany) minus the conditioned medium from 5637 bladder carcinoma cell line. The cytokines were refreshed at day 3. Further differentiation to MUTZ3 mDCs was achieved by addition of 10 ng/mL LPS (Sigma-Aldrich, Germany) at day 7 and culturing for additional 48-72 hours. To generate the THP1-derived macrophages (THP1MΦ), THP1 cells were differentiated in the presence of 50 ng/ml phorbol 12-myristate 13-acetate (PMA) (Sigma, Steinheim, Germany) for 48 hrs. Subsequently, for LC-MS/MS the MUTZ3 iDC, MUTZ3 mDC and THP1MΦ cells were harvested by 10 min centrifugation at 800 x g, shock-frozen in liquid nitrogen and stored as pellets at -80°C.

2.4 MUTZ3 iDC, MUTZ3 mDC and THP1MΦ phenotype analysis by flow cytometry

DC and macrophage phenotypes were assessed by flow cytometry. 1 x 10^5 MUTZ3 iDC and MUTZ3 mDC cells were stained with fluorochrome-labeled monoclonal antibodies against CD80, CD83, CD86, HLA-ABC, HLA-DR (BD Bioscience, Heidelberg, Germany) and HLA-A2 (BioLegend, Eching, Germany). 1 x 10^5 THP1MΦ cells were stained against HLA-ABC (BD Bioscience, Heidelberg, Germany) and HLA-DR (BioLegend, Eching, Germany). The expression of these markers on the surface of the DCs and THP1MΦ was determined with a FACSCalibur flow cytometer (Becton Dickinson, Heidelberg, Germany); and the data were processed and analyzed using CellQuest (Becton Dickinson, Heidelberg, Germany) and WinMDi 2.9 (Purdue University, USA) software, respectively. The macrophage phenotype was also confirmed by adherence of THP1MΦ to the T 25 cm^2 cell culture flask (Nunc, Wiesbaden, Germany).

2.5 THP1MΦ infection with *Leishmania donovani*

To infect THP1MΦ with the BHU5 or YFP-BHU5, parasites were harvested by centrifugation at 500 x g for 8 minutes, washed, re-suspended in RPMI 1640 medium (Invitrogen, Karlsruhe, Germany) and added to the THP1MΦ refreshed cultures in the ratio parasites:THP1MΦ 10:1, and cultured for 48 h at 37°C under 8% CO_2. Subsequently, THP1MΦ and YFP-BHU5 infected THP1MΦ (THP1MΦi-y) were used immediately to access the uptake of YFP-BHU5 by THP1MΦ and its effects on HLA-ABC and HLA-DR expression. THP1MΦ and BHU5 infected THP1MΦ (THP1MΦi) were used to access viability, HLA-ABC, HLA-A*02:01 and CD83 expression, and were harvested by 10 min centrifugation at 800 x g, shock-frozen in liquid nitrogen and stored as pellets at -80°C for isolation of HLA.

2.6 Parasite uptake, viability, activation and HLA expression

To determine the uptake of LD by THP1MΦ and effects on hosts viability, CD83, HLA-ABC, HLA-A*02:01 and HLA-DR expression flow cytometry was used. THP1MΦ and THP1MΦiy or THP1MΦi were stained with fluorochrome-labeled monoclonal antibodies against CD11b, CD83, HLA-ABC (BD Bioscience, Heidelberg, Germany), HLA-A*02:01 and HLA-DR (BioLegend, Eching, Germany), Calcein-AM (Invitrogen, Eugene, Oregon, USA) and Propidium Iodide (PI) (Sigma-Aldrich, Steinheim, Germany). The expression of these markers on the cell surface and of calcein and PI fluorescence was determined with a FACSCalibur flow cytometer (Becton Dickinson, Heidelberg, Germany). CellQuest (Becton Dickinson, Heidelberg, Germany) and WinMDi 2.9 (Purdue University, USA) software were used to process and analyze the data, respectively. The uptake was assessed by CD11b expression against YFP fluorescence, and cell viability assessed using Calcein-AM Invitrogen, Eugene, Oregon, USA) and propidium iodide (PI) (Sigma-Aldrich, Steinheim, Germany). CD83 was used as a marker of macrophage activation.

2.7 Total RNA isolation and cDNA synthesis

Total RNA was extracted from THP1MΦ, THP1MΦi, HeLa cell line, and HeLa clone 33/2 (A2+/IP) using Nucleospin RNA II Purification Kit (Macherey-Nagel, Duren, Germany) as per the manufacturer's instructions. 1 x 10^6 cells were put in 2ml eppendorf tubes and lysed with 350 µl lysis buffer. Samples were centrifuged and the supernatant was mixed with 350µl (70%) ethanol and centrifuged through a nuceospin RNA column, to bind the RNA to the silica gel membrane. Traces of DNA were removed by DNAse treatment. DNAse and any contaminant were washed away with wash buffer and RNA was eluted in RNase-free water. RNA concentration was measured at room temperature with a UV/VIS spectrophotometer (Perkin Elmer, Germany) according to manufacturer's instruction with 1µl of the RNA sample diluted 50 times with RNase-free water. cDNAs were synthesized from 500 ng each of the DNase-

treated total RNA using superscript III reverse transcriptase kit (Invitrogen, CA, USA) as per the manufacturer's instructions. cDNA-3' Primer (AAG CTG TGG TAA CAA CGC AGA GTC GAC TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT VN) was used in a cDNA synthesis mixture containing (20 µl) 5x First strand Buffer, (4 µl) 0.1 M DTT , 200 U superscript III reverse transcriptase enzyme, 20 pmol cDNA-3' primer, 10 mM dNTP mix and 500 ng RNA. The cycling condition comprised of denaturation at 65°C for 5 minutes, annealing and cDNA synthesis at 50°C for 60 minutes and termination at 72°C for 15 minutes.

2.8 Constitutive and immunoproteasome expression in THP1MΦ and THP1MΦi

The impact of the infection by LD on the constitutive and immunoproteasome expression of THP1MΦ was determined by semi-quantitative RT-PCR. RT-PCR was carried out with 500 ng of THP1MΦ, THP1MΦi, HeLa cell line, and HeLa clone 33/2 (A2+/IP) of each cDNA using the following constitutive (β1, β2 and β5) and immunoproteasome (β1i, β2i and β5i) subunits, and GADPH-sequence specific forward and reverse primers (114). β1: GACTCCAGAACAACCACTG, CTTGGTCATGCCTTCCCG (399 bp; BC000835.2, NM_057099.2); β2: CTGAAGGGATGGTTGTTGC, CTTTCTCACACCTGTACCG (558bp; D38048.1, NM_053532.1); β5: CCAAACTGCTTGCCAACATG, GAGTAGGCATCTCTGTAGG (275 bp; D29011.1, XM_341314.3); Hsβ1i: CTACTGTGCACTCTCTGG, GCCTGGCTTATATGCTGC (313 bp; U01025); Hsβ2i: GAAGATCCACTTCATCGC, CTCCAGGGTTAGTGGCTTC (571 bp; Y13640); Hsβ5i: GGAGAAAGGAACGTTCAG, TTGATTGGCTTCCCGGTAC (648 bp; U17496); GAPDH: CCTTCATTGACCTCAACTAC, CACCACCCTGTTGCTGTAG (869 bp; NM_002046.2, NM_017008.2). Each RT PCR setup contained (5 µl) 10x Dream Taq green buffer (Thermoscientific, Darmstadt, Germany), (2 µl) 2.5 mM dNTP mix, (0.5 µl) of each 30 pmol/µl GADPH-sequence specific forward and reverse primers, (1 µl) of each 100 pmol/µl constitutive or immunoproteasome subunits sequence specific forward and reverse primer, 500 ng cDNA,

15,875 µl PCR grade water and 0.125 µl Dream Taq DNA polymerase (Thermoscientific, Darmstadt, Germany). PTC-200 Peltier Thermal Cycler (BIO-RAD, München, Germany) was used and thermo-cycling conditions were denaturation at 96°C for 2 min, 30 cycles of denaturation at 95°C for 40 sec, primer annealing at 55°C to 68°C for 1 min, primer extension at 72 °C for 40 sec and a final cycle of extension at 72°C for 10 min. The amplified DNA fragments were analyzed by electrophoresis using 1% agarose gels in 1 x TBE buffer with 0,006 % ethidium bromide (Roth, Karlsruhe, Germany). HeLa cell line, and HeLa clone 33/2 ($A2^+$/IP) were used as positive controls for constitutive and immunoproteasome subunits respectively. GelAnayzer2010 (http://www.gelanalyzer.com/download.html) was use to semi-quantitatively analyze the subunit band intensities. For each subunit, the band intensity was divided by the value for the GAPDH amplified in the same reaction tube.

2.9 Statistical analyses for macrophage activation, HLA and proteasome subunits expression

Macrophage activation, HLA expression and proteasome subunits expression between THP1MΦ and THP1MΦi/or THP1MΦiy were compared by paired 1-tailed student's t-test and differences indicated as significant when *$p < 0.05$. Data are presented as the mean ± standard deviation from three independent experiments.

2.10 Isolation and purification of MHC I-presented peptides

MHC class I molecules were isolated as described in (115-117). (2.4×10^9) MUTZ3 iDC, (2.1×10^9) MUTZ3 mDC, (2.8×10^9) THP1Mϕ and (2.3×10^9) THP1Mϕi cells were lyzed each in 20 mM Tris-HCl buffer (Sigma, Steinheim, Germany), pH 7.4, 0.3% CHAPS (Roth, Karlsruhe, Germany), 0.2% NP-40 (Thermo Scientific, Bonn, Germany), 145 mM NaCl (Sigma, Steinheim, Germany), 1 mM EDTA (Merck, Darmstadt, Germany), 1mM Pefabloc (Roche, Mannheim, Germany). Lysates were ultracentrifugated for 1 hr at 100,000 x g and the supernates passaged through a column with 19-1.78 monoclonal antibody of irrelevant

specificity followed by a column with the monoclonal anti-human HLA-I antibody W6/32, both coupled to activated CH Sepharose (Amersham Biosciences, Uppsala, Sweden) as per manufacturer's protocol. After adsorption of the proteins, the anti-human HLA-I column was washed with the following in descending order; 20 mM Tris, 145 mM NaCl, pH 7.4 (TBS), 0.3% CHAPS in TBS, TBS, 0.3% ß-octylglycoside (Roche, Mannheim, Germany) in TBS, TBS and finally with ultrapure water. HLA-peptide complexes were eluted from the column with 0.7 % TFA (Sigma, Steinheim, Germany) in ultrapure water. High molecular weight components were separated from peptides by centrifugal ultrafiltration using a 3 kDa molecular weight cut-off (Centricon, Millipore, Schwalbach, Germany). The filtrates were fractionated on a Smart HPLC system (Amersham Biosciences, Freiburg, Germany) using a reverse phase column µRPC C2/C18, SC2.1/10 (Amersham Biosciences, Freiburg, Germany) and an acetonitrile (Sigma-Aldrich, Steinheim, Germany) gradient of 5 - 90% of B (solvent B: 90% of acetonitrile, 0.1 % TFA; solvent A: 0.1% TFA in ultrapure water). The fractions obtained were lyophilized in vacuum centrifuge/speed vac (Thermo Savant, Sant Jose, USA) and re-dissolved in 12 µl of 0.1% TFA 2% acetonitrile for LC-MS/MS.

2.11 LC-MSMS analysis of HLA ligands

The peptides fractions were analyzed by reverse phase liquid chromatography using the Ultimate 3000 nano-HPLC system (Dionex, Darmstadt, Germany) coupled on-line to MicrOTOF-Q ESI-QTOF mass spectrometer (Bruker Daltonics, Bremen, Germany). Peptide fractions were loaded onto a C18 precolumn at a flow rate of 20 µL/min in 98% solvent A (1% acetonitrile, 0.1% FA) for 5 minutes, and then onto a PepMap nano-HPLC column (75µm×15cm i.d.) (LC Packings, The Netherlands) at a flow rate of 220 nL/min and 2% solvent B (95% acetonitrile, 0.1% FA) and 98% solvent A. A gradient of 5-60% of B over 60 min, then 60-90% of B over 5 min and finally 90 % of B for 5 min was used to elute the peptides. The MicrOTOF-Q ESI-QTOF masspectrometer was controlled by MicrOTOF control software,

version 2.2 (Bruker Daltonics) and operated in a data-dependent mode. Fragmentation of peptides was done on the five most intensive signals using optimized collision energy. A dynamic exclusion time of 1 min was used to avoid repeated fragmentation of the most abundant precursors.

2.12 LC-MS/MS data processing and analysis

The processing of the MS and MS/MS spectra was done using Data Analysis 3.4 and Biotools 3.1 software (Bruker Daltonics). The peptides were identified by a local MASCOT server (version 2.2), using the Swissprot databank version 56.3 for human proteins (20,408 entries), a precursor mass tolerance of 50 ppm, and 100 ppm for MS/MS, and oxidation of methionine as possible modification. For each peptide-spectrum match, candidate sequences were validated using a statistical evaluation -10logP, where logP is the logarithm to the base 10 of P ($P<0.05$) as the absolute probability. Further validation of the identified peptides on the basis of *de novo* sequencing was done using the Sequit software (107), and by manual inspection of the peptide-spectrum. The protein sequence, protein ID and gene symbol for proteomic data analyses were extracted from Uniprot database (118). The human protein reference database (119) was used to classify proteins according to their subcellular localizations and biological function. HLA assignment of the peptides was done on the basis of canonical binding motifs, using SYFPEITHI (120) and immune epitope database IEDB (121,122).Visualization of the binding motifs for HLA-A*02:01, HLA A3, HLA B44 molecules for the nonapeptides derived from the MUTZ3 iDC and MUTZ3 mDC, and HLA-A*02:01, HLA-C*03:03 and HLA-B*15:11 from THP1MΦ and THP1MΦi was done using sequence logos (123,124). Artificial neural networks (ANN) or netMHCpan in IEDB (121,122,125,126) was used to assign the HLA binding affinities to the peptides.

2.13 Peptides

Published clinically validated leukemia tumour associated antigens (TAAs) HLA-A*02:01 epitopes **(Table 2)**, and HLA-A*02:01 peptides identified from MUTZ3 DCs and THP1MΦ HLA class I–peptidomes from potential leukemia TAAs (TAAs that have been described in other solid and hematological malignancies); and HIV polymerase peptide **(Table 3)** were synthesized by EMC microcollections GmbH (Tubingen, Germany) with a purity >95%. Lyophilized peptides were dissolved in DMSO (Pierce, Rockford, Illinois, USA) and stored at -20°C. The binding affinity of these peptides was determined using T2 cell line HLA-A*02:01 binding assay, and by prediction using ANN in IEDB (121,122).

Table 2. Published clinically validated leukemia TAAs HLA-A*02:01 epitopes.

Protein	**Peptide**	**Sequence**	**Immunogenicity and clinical relevance (Reference)**
hTERT	P540_hTERT	ILAKFLHWL	(127,128)
PRAME	P300_PRAME	ALYVDSLFFL	(129-133)
WT1	P187_WT1	SLGEQQYSV	(134,135)
RHAMM	P165_RHAMM	ILSLELMKL	(132,136-138)
PROTEINASE 3	P169_PROTEINASE 3	VLQELNVTV	(139,140)

Table 3: Potential Leukemia TAAs HLA-A*02:01 epitopes derived from MUTZ3 DCs & THP1MΦ HLA-I peptidome; and HIV polymerase peptide

Protein	Peptide	Sequence	Peptide Source	Protein role in cancer (Reference)
MBOA7	P141_MBOA7	GLLPDVPSL	MUTZ3 iDC	(141-143)
LARP1	P130_LARP1	ALPPVLTTV	MUTZ3 mDC	(144,145)
TRRAP	P378_TRRAP	TLADLVHHV	MUTZ3 mDC	(146-148)
PININ	P207_PININ	RLLEQKVEL	THP1MΦ	(149-151)
ROS1	P308_ROS1	HLVDEAHCLRL	THP1MΦ	(152-156)
PSME3	P114_PSME3	QLVDIIEKV	THP1MΦ	(157)
URP2	P326_URP2	ALSNLEVKL	THP1MΦ	(158,159)
UHRF1	P57_UHRF1	TLFDYEVRL	THP1MΦ	(160,161)
HIV Polymerase*	P564_HIVPol	LLFGXPVYV		

*Used as positive control for T2 cell line HLA-A*02:01 binding assay

2.14 T2 cell line HLA-A*02:01 binding assay

To determine the HLA-A*02:01 binding affinity of each peptide in Table 2 and 3, TAP-deficient HLA-A*02:01-positive T2 lymphoma cell line was used as previously described (162) with slight modifications. 2 x 10^5/ml of TAP-deficient HLA-A*02:01 -positive T2 lymphoma cell line were seeded in DMEM (Gibco-BRL, Karlsruhe, Germany) with 2 µg/ml β2-microglobulin (Sigma-Aldrich, Steinheim, Germany) and incubated with 100 µM sequence specific peptides for 18hrs at 37°C and 8% CO2. After incubation, cells were harvested by centrifugation at 400 x g for 7 min, washed with PBS (Gibco, Grand Island, NY,USA) re-suspended in 200 µl PBS (Gibco, Grand Island, NY,USA) and incubated with anti- human HLA-A2 FITC clone BB7.2 mAb (BioLegend, Eching, Germany) for 45 min at 4°C. Cells were

then washed with 500 µl PBS (Gibco, Grand Island, NY, USA) and re-suspended in 400 µl PBS (Gibco, Grand Island, NY, USA). Fluorescence intensity was measured using FACSCalibur flow cytometer (Becton Dickinson, Heidelberg, Germany), and the data were processed and analyzed using CellQuest (Becton Dickinson, Heidelberg, Germany) and WinMDi 2.9 (Purdue University, USA) softwares. The P564_HIVpol peptide in Table 3 was used as positive control and T2 cells without peptide as a negative control.

2.15 PBMCs from Healthy Volunteers

The clinical material was used with approval by Charite' ethics committee (Approval No. EA1/222/14 and EA1/026/14) and written informed consent by Volunteers. HLA typing was carried out by the HLA typing laboratory, Charite' University, Berlin. PBMCs were isolated from peripheral blood of 4 HLA- A*02:01 positive Healthy Volunteers by density centrifugation using Ficoll Paque (density 1.077 g/ml) (Biochrom, Berlin, Germany). To isolate the PBMCs, blood was diluted with an equal volume of PBS (Gibco, Grand Island, NY,USA) and layered on top of 15 ml Ficoll solution (Biochrom, Berlin, Germany) using a 50 ml falcon tube. A ficoll gradient was created by centrifuging for 20 minutes at 1000 x g at room temperature, with the brake off. PBMCs were collected from the Ficoll: plasma interface, washed twice with PBS (Gibco, Grand Island, NY, USA) and cryopreserved in FCS (Biochrom, Berlin, Germany) with 10% DMSO (Pierce, Illinois, USA) at -140°C. For in vitro priming, thawed PBMCs from the 4 healthy donors were pulsed individually with 10 µg/ml of each peptide in ExVivo 15 serum-free medium (Biowhitaker, Belgium) at 37°C and 8% CO2. 50 U/ml of recombinant human IL-2 (Chiron, München, Germany) was added to the cultures on day 1, and day 3. On day 8 the primed PBMCs were harvested, washed with PBS (Gibco, Grand Island, NY, USA) and counted before analysis using INFγ ELISpot assay.

2.16 IFNγ ELISpot Assay

2.5 x 10^5 primed PBMCs from 4 healthy donors were pulsed individually with 10 µg/ml of each peptide in ExVivo 15 serum-free medium (Biowhitaker, Belgium) in 96 well multiscreen plates (Milipore, Darmstadt, Germany) coated overnight at 4°C with 100 µl (1:1000) of anti-human INFγ capture monoclonal antibody (Endogene, Pierce Biotechnology, Inc). PBMCs pulsed with Phytohaemagglutinin (PHA) (2.5 µg/ml) (Sigma-Aldrich, Steinheim, Germany) and PBMCs with culture medium only were used as positive and negative control respectively. ELISpot plates were incubated for 18 hrs hours at 37°C and 8% CO_2. Plates were then washed twice with PBS (Sigma-Aldrich, Steinheim, Germany) and incubated with 50 µl (1:500) biotinylated anti-human IFN-γ antibody (Endogene, Pierce Biotechnology) for 2 hrs at room temperature (RT). Following washing twice with PBS (Gibco, Grand Island, NY, USA), plates were incubated with 50 µl streptavidin-conjugated with alkaline phosphatase (1:2000) (Roche, Mannheim, Germany) for 1 hr at RT and washed 3 times with 100 µl PBS (Gibco, Grand Island, NY,USA) followed by 50 µl BCIP/NBT (5-Bromo-4-chloro-3-indolyl phosphate/Nitro blue tetrazolium) substrate for 30 min as per manufacturer's instructions (Moss Inc., Pasadena, CA, USA). ELISpot plates were dried overnight at 4 °C and thereafter scanned and counted using Bioreader 3000 (BioSys, Karben, Germany).

3. Results

3.1 MUTZ3-derived immature and mature DCs and THP1-derived macrophages phenotypes

After differentiation of MUTZ3 cell line to MUTZ3 iDC and MUTZ3 mDC their phenotypic status was determined by measuring the expression of DCs maturation markers CD83, CD80, CD86, HLA DR, HLA ABC, and HLA-A*02:01 by flow cytometry. The maturation markers were expressed in both MUTZ3 iDC and MUTZ3 mDC, to a slightly greater extent in the mature DC phenotype **(Figure 8A).** The expression of these maturation markers in both DC phenotypes was in agreement to previous reports (92,163). The differentiation of THP1 to macrophages was ascertained by the adherence of THP1MΦ to the surface of the cell culture Flask (**Figure 8B)** and expression of HLA DR and HLA ABC (**Figure 8C**)

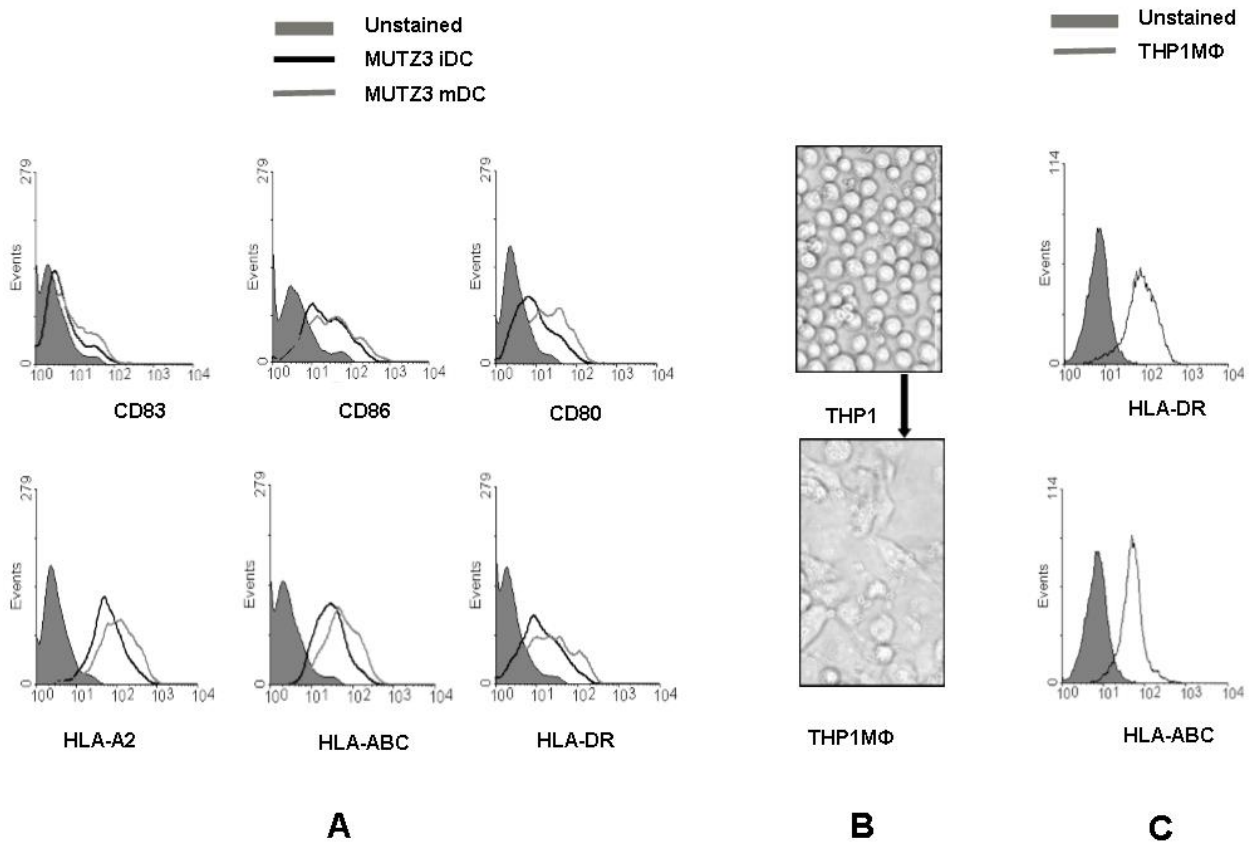


Figure 8: DC and macrophage differentiations. A) A representative of analysis of MUTZ3 iDC and MUTZ3 mDC phenotypes. MUTZ3 iDCs were generated by culturing the MUTZ3 cells as detailed in

material and methods, after which the MUTZ3 mDC were generated by addition of LPS. Expression levels of CD80, CD86, CD83, HLA ABC, HLA-A*02:01, and HLA-DR on the surface of both MUTZ3 iDC and MUTZ3 mDC were analyzed by flow cytometry. **B)** Acquisition of an adherent phenotype by THP1 upon differentiated to THP1MΦ after exposure to PMA. **C)** Expression levels of HLA-DR and HLA ABC in THP1MΦ

3.2 Naturally presented HLA I ligands in MUTZ3 DCs and THP1MΦ

MUTZ3 iDC, MUTZ3 mDC and THP1MΦ cells were lysed, and MHC class I molecules isolated by affinity chromatography, and peptides extracted from the MHC molecules analyzed by LC-MS/MS. The sequences of a total of 327, 301 and 347 HLA class I-bound peptides were identified from 297, 273 and 282 source proteins in MUTZ3 iDC, MUTZ3 mDC and THP1MΦ respectively **(Supplementary table 1)**. Though the MUTZ3 iDC and MUTZ3 mDC are derived from the same cell line and have the same HLA-I alleles, only 59 and 74 HLA I peptides sequences were found to be shared between them based only on peptide sequences, and precursor peptide masses signals and retention times respectively. MUTZ3 iDC and MUTZ3 mDC express HLA-A*02:01, HLA-A3, HLA-B44 and HLA-B56, THP1MΦ HLA-A*02:01, HLA-C*03:03 and HLA-B*15:11 (92,109-111). In reference to HLA-A*02:01, a total of 77, 99 and 122 HLA-A*02:01 restricted peptides were identified from MUTZ3 iDC, MUTZ3 mDC and THP1MΦ respectively. Only 12 and 18 of these peptides were found to be shared between MUTZ3 iDC and MUTZ3 mDC, 8 and 13 between THP1MΦ and MUTZ3 iDC, 8 and 11 between THP1MΦ and MUTZ3 mDC, and 2 among MUTZ3 iDC, MUTZ3 mDC and THP1MΦ, based on peptide sequences, and precursor peptide masses signals and retention times respectively. In reference to the source proteins of the identified peptides, 64 source proteins were found to be shared between the MUTZ3 iDC and MUTZ3 mDC, 10 between THP1MΦ, MUTZ3 iDC and MUTZ3 mDC, 15 between THP1MΦ and MUTZ3 iDC, and 15 between THP1MΦ and MUTZ3 mDC **(Figure 9)**

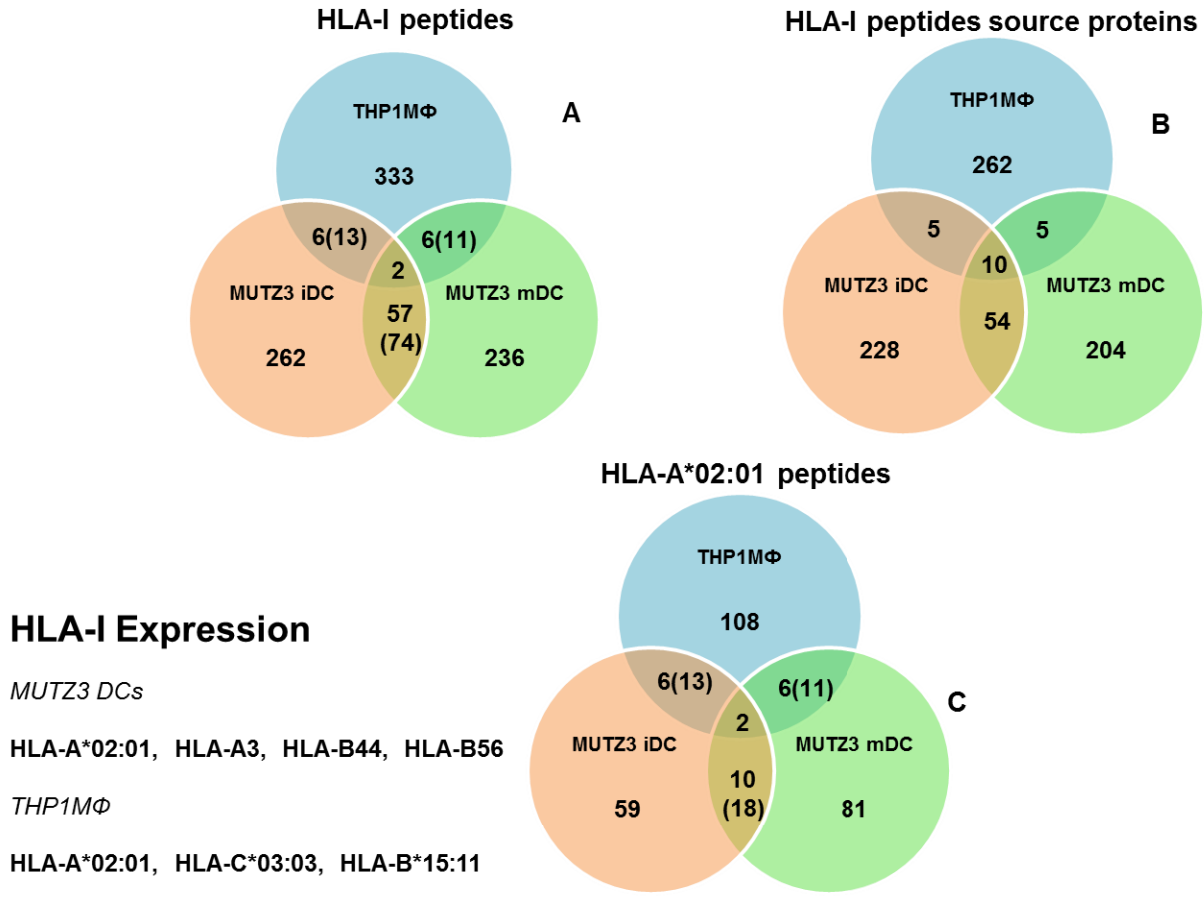


Figure 9. Overlap in HLA-I peptides and source proteins in MUTZ3 iDC, MUTZ3 mDC and THP1MΦ

3.3 MHC I-bound peptide lengths in MUTZ3 DCs and THP1MΦ

The MHC I-bound peptide lengths in both DCs and the macrophage phenotypes were dominated by nanopeptides with 55 to 57% of all the identified peptides. The dominance of nanopeptides was also observed in the shared peptides between MUTZ3 iDC and MUTZ3 mDC, and in the HLA-A*02:01-bound peptides shared among the MUTZ3 DCs and THP1MΦ. This dominance of nanopeptides has also been observed in other cell lines, and patient tumor samples (117,164-166), and indicates that nine amino acids is the optimum length for MHC I-binding peptides. Decapeptides were the second dominant, and constituted 22% and 25% for MUTZ3 iDC and MUTZ3 mDC, and 12% for THP1. Undecapeptides and above, on the other hand were less than 2% in both MUTZ3 iDC and MUTZ3 mDC, and 6% in THP1MΦ **(Figure**

10). The percentages of undecapeptides were very similar between the MUTZ3 DCs, as compared to those of THP1MΦ whereas the share of decapeptides among all HLA I-bound peptides from THP1MΦ it is only half of what was found for the MUTZ3 DCs.

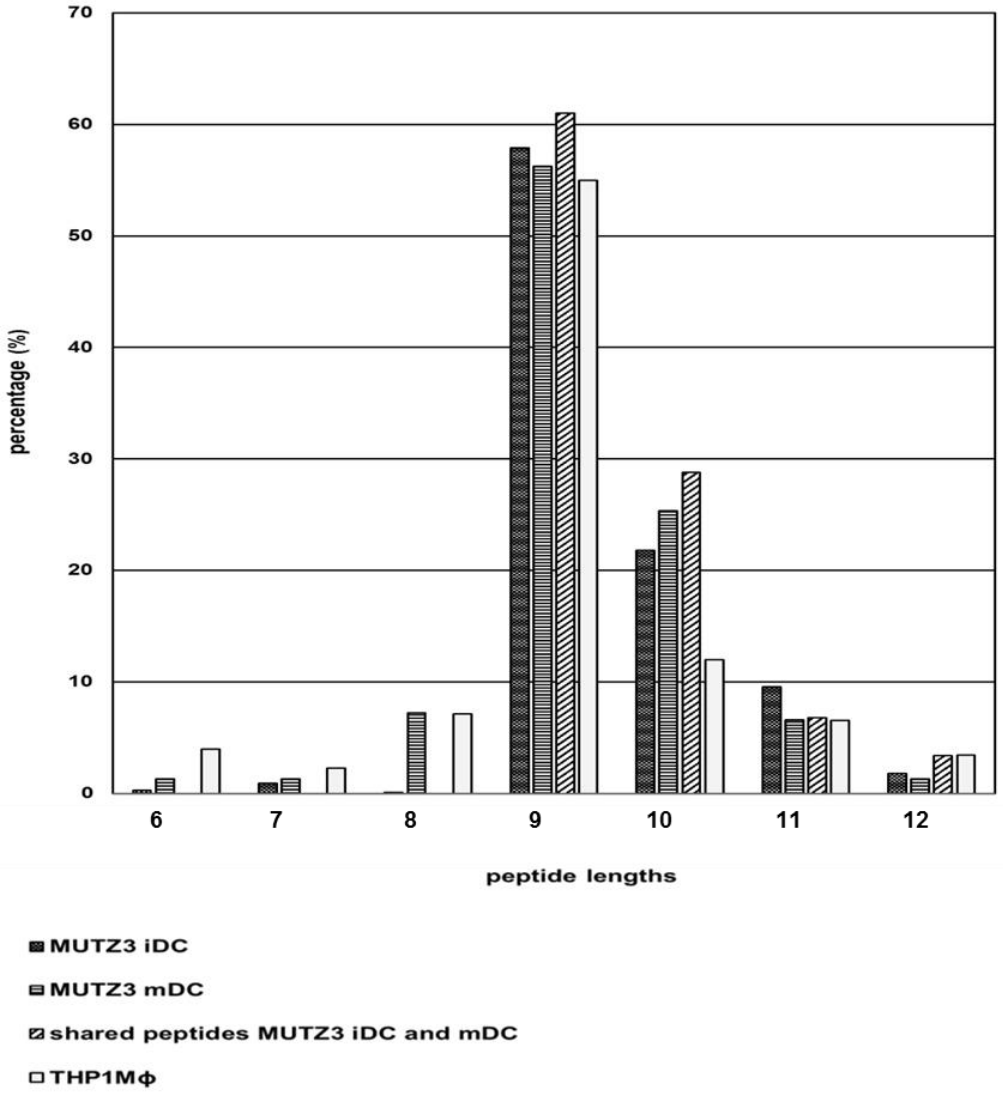
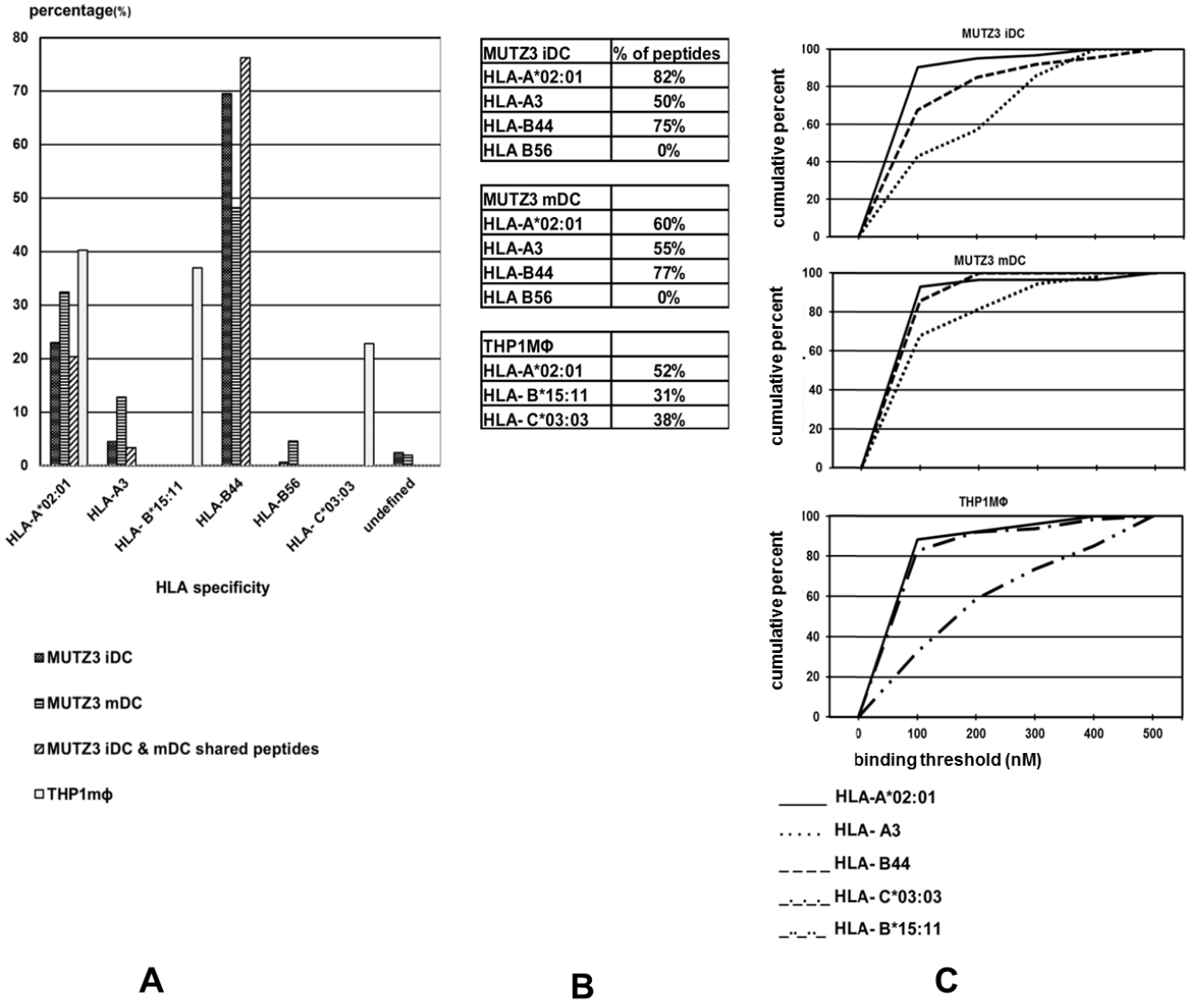


Figure 10: MHC Class I -peptide lengths in MUTZ3 iDC, MUTZ3 mDC and THP1MΦ.

3.4 HLA allomorph assignment and binding affinities of peptides in MUTZ3 DCs and THP1MΦ

We utilized canonical peptide binding motifs listed in the SYFPEITHI database (120) and ANN in IEDB (121,122) for the respective HLA class I to identify the MHC restriction of the peptides. For MUTZ3 iDC 70%, 23%, 4%, and 1% of the peptides were assigned to HLA-B44, HLA-A*02:01, HLA-A3, and HLA-B56, respectively, and 48%, 32%, 13%, and 5% to MUTZ3 mDC. Approximately 2% of the peptides in both DC phenotypes were unassigned **(Figure 11A).** In THP1MΦ 40%, 37% and 23% of the peptides were assigned to HLA-A*02:01, HLA-C*03:03 and HLA-B*15:11, respectively. In both MUTZ3 DC phenotypes, the percentages of peptides assigned were in the order HLA-B44≥ HLA-A*02:01 ≥ HLA-A3≥ HLA-B56. To determine what percentage of the identified MHC-1 peptides (8-14mers) had biological significant binding affinity, we used ANN in IEDB (121,122) and applied a binding affinity IC_{50} threshold of 500 nM, which was established previously for known T cells epitopes, and had been shown to correlate with immunogenicity (167). In MUTZ3 DCs, the percentage of peptides that were within this threshold was relatively the same across all the alleles, and the difference was only seen in HLA-A*02:01 peptides, where the percentages were higher in MUTZ3 iDC (82%) as compared to MUTZ3 mDC (60%). No peptides were within this threshold for HLA-B56. In THP1MΦ the highest percentage of peptides was seen in HLA-A*02:01 (52%) **(Figure 11B).** The cumulative percentage frequencies for HLA-A*02:01 and HLA-B44 peptides in MUTZ3 DCs were the same, but there was a shift towards higher affinity peptides for HLA-A3 in MUTZ3 mDCs. In reference to the HLA-A*02:01-bound peptides in MUTZ3 DCs and THP1MΦ, at IC_{50} threshold of 100nM the cumulative percentage frequencies were similar, and all above 82% **(Figure 11C).**



MUTZ3 iDC	% of peptides
HLA-A*02:01	82%
HLA-A3	50%
HLA-B44	75%
HLA B56	0%

MUTZ3 mDC	
HLA-A*02:01	60%
HLA-A3	55%
HLA-B44	77%
HLA B56	0%

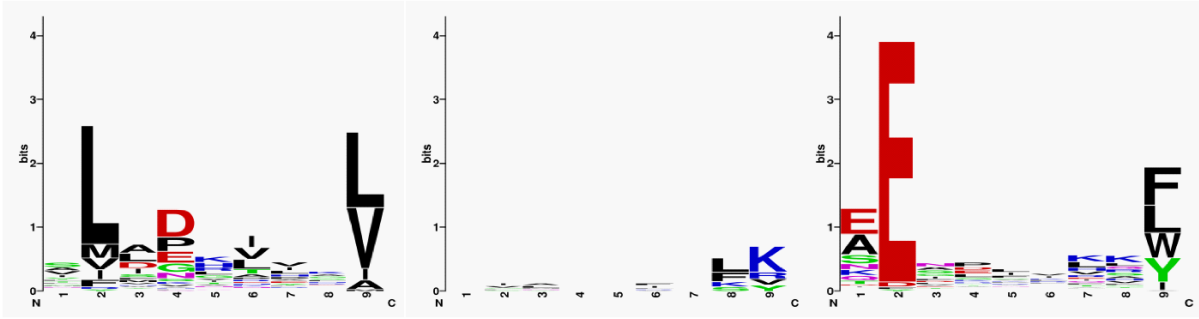
THP1MΦ	
HLA-A*02:01	52%
HLA- B*15:11	31%
HLA- C*03:03	38%

Figure 11: HLA restriction and binding affinities. A) MHC restriction of HLA I-bound peptides from immature and mature DC phenotypes were assigned using the canonical binding motif according to SYFPEITHI and ANN in immune epitope database (IEDB). **B)** Percentage of MUTZ3 iDC and MUTZ3 mDC and THP1MΦ HLA peptides with an IC_{50} ≤500nM. **C)** Cumulative percent of MHC I peptides in MUTZ3 iDC and MUTZ3 mDC and THP1MΦ at an IC_{50} threshold of 500 nM.

3.5 The binding motifs for HLA-I molecules in MUTZ3 DCs and THP1MΦ

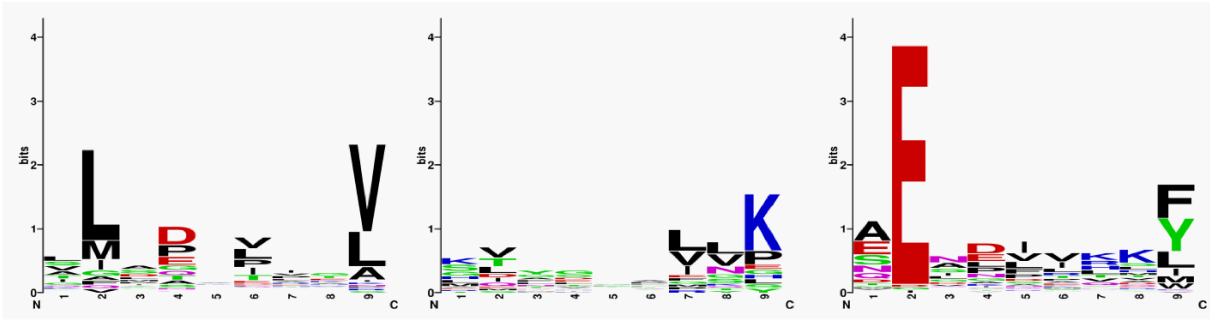
We further determined whether there was a particular preference for binding motifs in the nanopeptides from MUTZ3 iDC, MUTZ3 mDC and THP1MΦ, using sequence logos (123,124). The height of each column of letters is equal to the information content (in bits) at the given positions in the peptide sequence, and the relative height of each letter within each column is proportional to the frequency of the corresponding amino acid at that position. The frequency of the primary anchor residues at position 2 and the C-terminus in the HLA-A*02:01, HLA-A3 and HLA-B44 nonapeptides, in both DC phenotypes was essentially the same, with only minor differences in the order and identity of residues at position 2 and the C-terminal positions. There was a high frequency of L and M at Position 2, and V and L at C terminus for HLA-A*02:01-bound peptides with V more prominent in P9 in case of the mDCs versus iDCs, E at P2 and K at C- terminus for HLA-A3 peptides, and aromatic amino acids at C-terminus for HLA B44-bound peptides **(Figure 12).** In THP1MΦ the frequency of L and I was high at P2, V and L at C-terminus for HLA-A*02:01-bound peptides, A and Y at position 2 and L and F at C terminus for HLA-C*03:03-bound peptides, P at position 2, and Y and F at the C-terminus for HLA-B*15:11-bound peptides **(Figure 12).** The frequency of the primary anchor residues at position 2 and the C-terminus of the HLA-A*02:01-bound peptides in both DCs and THP1MΦ was essentially the same, and only minor differences were observed in the order and identity of residues at position 2 and the C-terminus.

MUTZ3 iDC



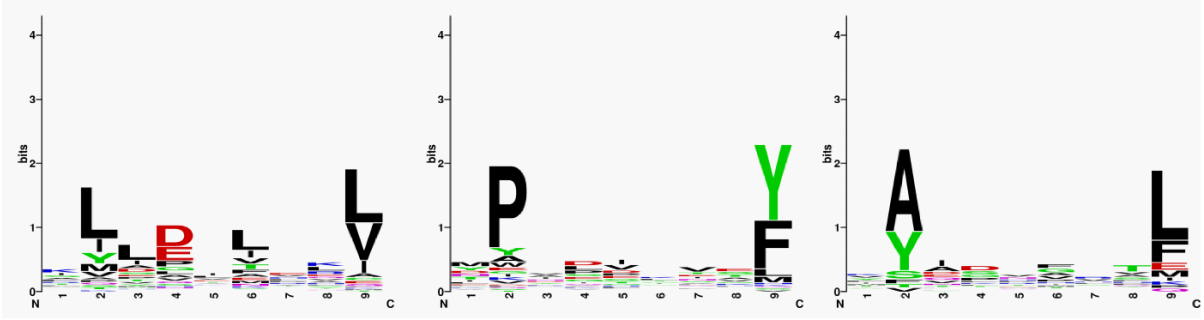
HLA-A*02:01 HLA-A3 HLA-B44

MUTZ3 mDC



HLA-A*02:01 HLA-A3 HLA-B44

THP1MΦ



HLA-A*02:01 HLA-B*15:11 HLA-C*03:03

Figure 12: The binding motifs for HLA-I molecules in MUTZ3 DCs and THP1Mϕ. Sequence logos displaying the binding motifs for HLA-A*02:01, HLA-A3- and HLA-B44-bound nonapeptides from MUTZ3 iDC and MUTZ3 mDc, and HLA-A*02:01, HLA-C*03:03- and HLA-B*15:11-bound nonapeptides from THP1MΦ. The height of each column of letters is equal to the information content (in bits) at the given sequence positions, while the relative height of each letter within the columns is proportional to the frequency of the corresponding amino acid at that position.

3.6 Subcellular locations and biological functions of the source proteins in MUTZ3 DCs and THP1MΦ

The human protein reference database was used to assign the subcellular location of the source proteins of the HLA I-bound peptides from MUTZ3 DCs and THP1MΦ. The nucleus, cytoplasm and the plasma membrane were the dominant subcellular locations of the source proteins **(Figure 13)**. Together, they accounted for 72%, 70% and 64% of all the source proteins in MUTZ3 iDC, MUTZ3 mDC and THP1MΦ, respectively. Approximately half of this percentage was solely from the nucleus, which accounted for more than 30% of all the source proteins. The other subcellular locations, endoplasmic reticulum, ribosome, membrane, nucleolus, mitochondrion, cytoskeleton, extracellular, golgi apparatus, lysosome, endosome, exosome, microsome and cytosol all together accounted for 24%, 24% and 31% of the source proteins in MUTZ3 iDC, MUTZ3 mDC and THP1MΦ, respectively. The subcellular location of 4%, 6% and 5% of the source proteins in the respective cells was unknown **(Figure 13).** There was no source protein found in intracellular vesicle compartments of MUTZ3 iDC, in the exosome and microsome compartments of the MUTZ3 mDC and in the microsome and nucleolus compartments of THP1MΦ.

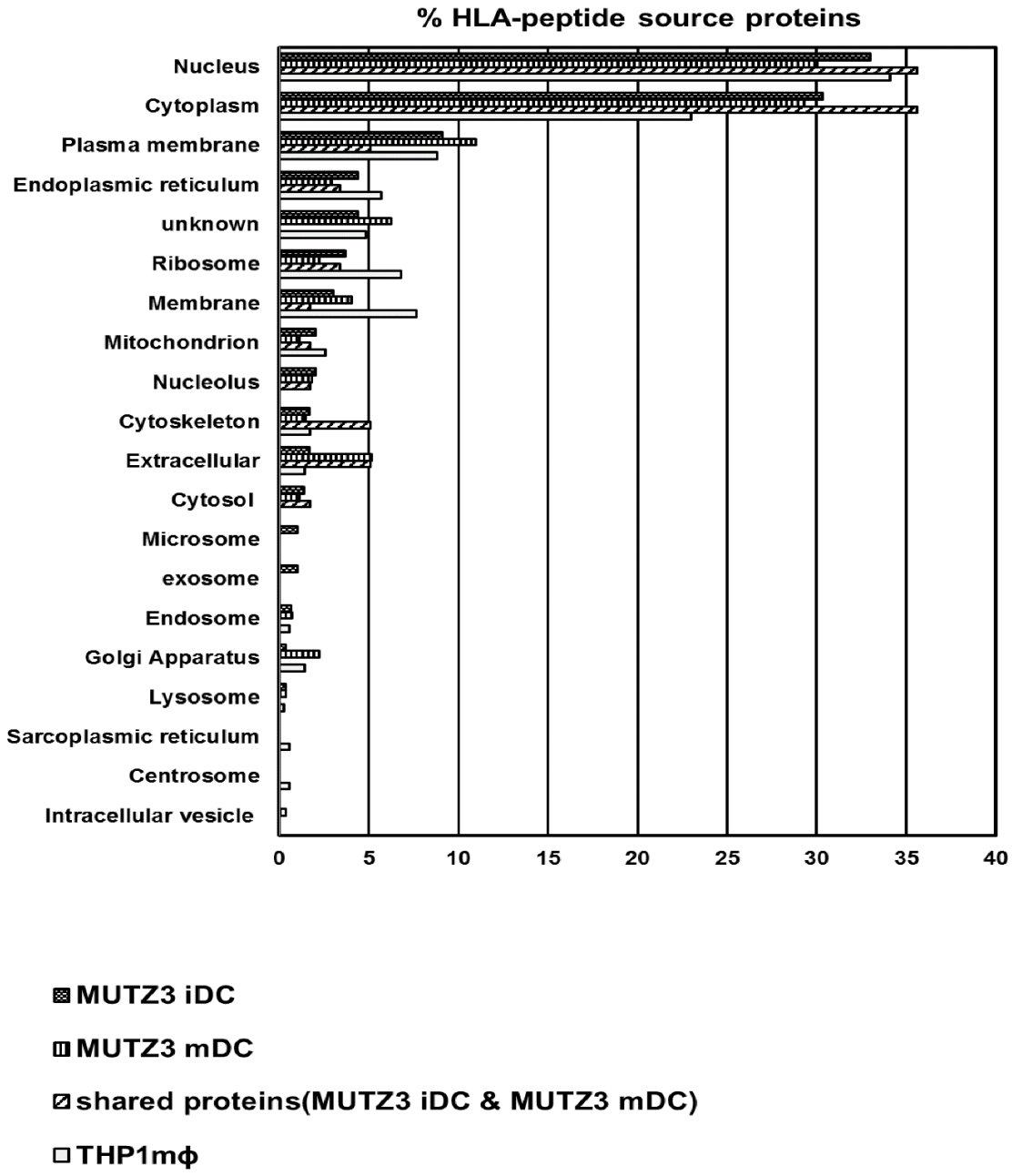


Figure 13: Subcellular location of the source proteins. The subcellular locations of the source proteins of the HLA class I-bound peptides from MUTZ3 iDC, MUTZ3 mDC, and THP1MΦ identified by mass spectrometry, were assigned using the Human Protein Reference Database.

The source proteins were further evaluated for their biological and molecular functions, again using the human protein reference database (119). Although source proteins possessed multiple biological functions, a vast majority of them in MUTZ3 iDC, MUTZ3 mDC and THP1MΦ were involved in cell communication/signal transduction (15%, 18%, 16%), protein metabolism

(15%, 12%, 19%) and transcription factor activity/regulator activity (12%, 12%, 11%), The remaining were involved in transport (6%, 8%, 8%), metabolism, energy pathways (8%, 8%, 6%), cell growth and/or maintenance (8%, 7%, 10%), immune response (5%, 3%, 2%), DNA binding (4%, 2%, 3%) and RNA binding (5%, 3%, 5%). Some were involved in other functions (13%, 7%, 5%), and some (8%, 14%, 7%) with no known biological functions. In reference to shared source proteins between MUTZ3 iDC and MUTZ3 mDC, these were involved in all biological functions, but mostly in cell growth and/or maintenance (14%) and cell communication/signal transduction (14%) **(Figure 14).**

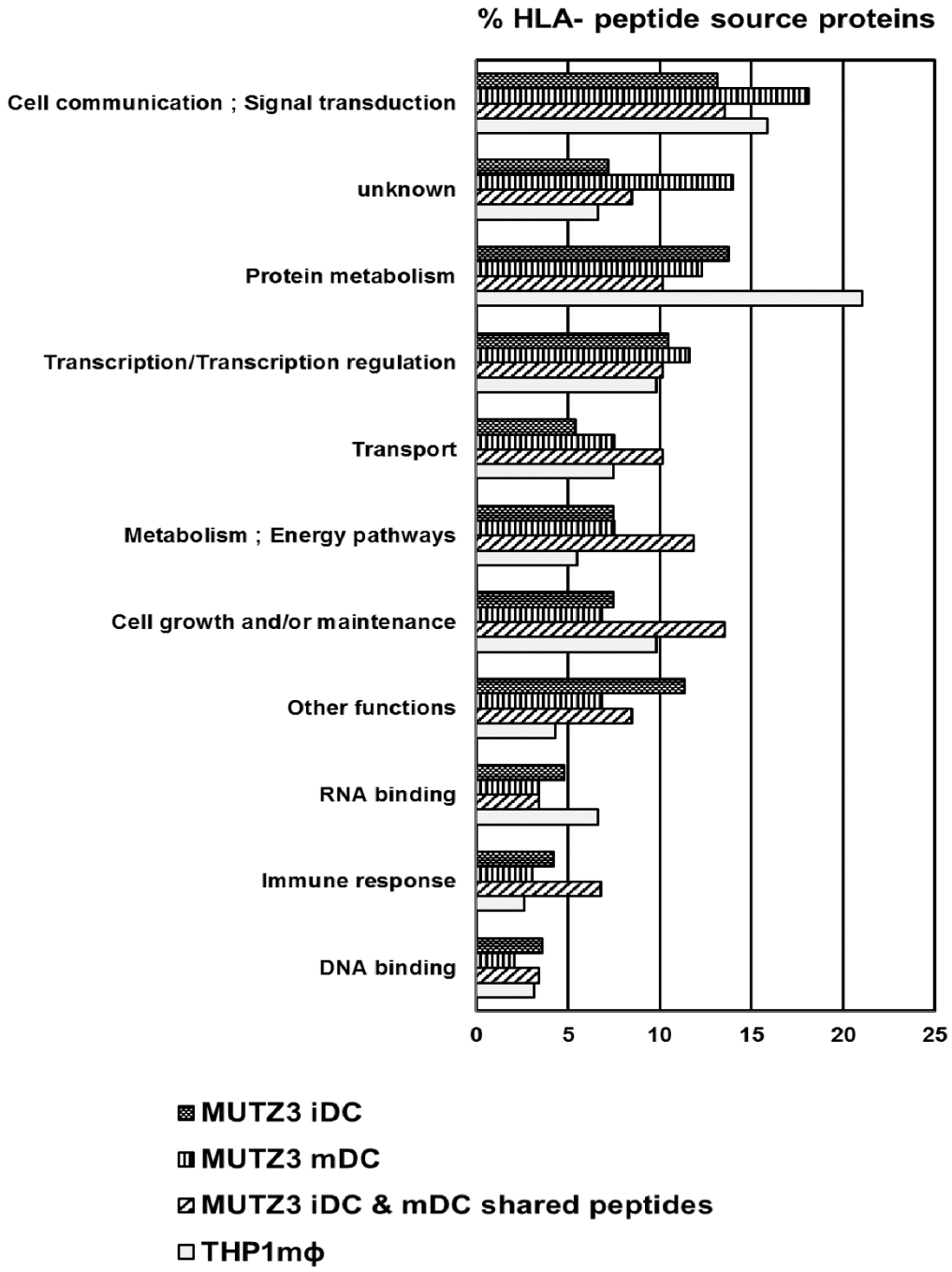


Figure 14: Biological and molecular functions of the source proteins. The biological and molecular functions of the source proteins of the HLA class I-bound peptides from MUTZ3 iDC, MUTZ3 mDC, and THP1MΦ, were assigned using the Human Protein Reference Database.

3.7 Potential TAAs epitopes in MUTZ3 DCs and THP1MΦ, and validation

HLA-A*02:01-bound peptides P141_MBOA7 from MUTZ3 iDC, P130_LARP1 and P378_TRRAP from MUTZ3 mDC, and P207_PININ, P308_ROS1, P114_PSME3,

P326_URP2 and P57_UHRF1 from THP1MΦ HLA class I–peptidomes **(Table 3)** were found to be derived from source proteins linked to some solid and other hematological malignancies **(Table 3)**. To validate these peptides as potential leukemia TAAs epitopes their binding affinities and ability to stimulate CD8+ T cells was determined in comparison to published immunogenic and clinically validated leukemia TAAs HLA-A*02:01 epitopes **(Table 2).** The T2 lymphoblastic cell line was used to determine the binding affinities in addition to prediction using ANN in IEDB. The T2 lymphoblastic cell lines are TAP deficient, and lack proper peptides to bind and stabilize the native conformation of the HLA class I molecules resulting in low cells surface expression of the HLA. Incubation with a suitable peptide stabilizes the HLA conformation resulting in increased HLA expression on the cells surface that is used as a measure of the peptide binding affinity. The peptide binding affinities based on the mean fluorescence intensity (MFI) values from three independent experiments was in the order; P141_MBOA7>P187_WT1>P57_UHRF1>P326_URP2>P169_PROTEINASE3>P300_PRAME>P540_hTERT>P130_LARP1>P378_TRRAP>P207_PININ>P308_ROS1>P114_PSME3>P165_RHAMM. With MFI values 249.31±21.31, 236.16±46.68, 215.82±19.62, 207.33±17.49, 181.31±42.47, 172.84±18.59, 171.74±16.67, 170.09±57.83, 161.77±33.39, 126.49±35.89, 116.25±25.63, 108.71±14.64 and 67.40±11.90 respectively. The MFI for P564_HIVPol (positive control) and without peptide (negative control) was 199.91±18.89 and 39.82±4.16 respectively. For all the test peptides the MFI was twofold and above that of negative control. **(Figure 15A).** The peptide binding affinities as predicted by ANN in IEDB using a binding affinity threshold of IC (500) nM was in the order; P378_TRRAP>P57_UHRF1>P540_hTERT>P141_MBOA7>P187_WT1>P169_PROTEINASE3>P300_PRAME>P130_LARP1>P114_PSME3>P207_PININ>P308_ROS1>P326_URP2>P165_RHAMM. With $1/IC_{50}$ (500) nM values of 0.25, 0.14, 0.14, 0.13, 0.10, 0.10, 0.09, 0.06, 0.04, 0.03, 0.01, 0.01 and 0.01 respectively (**Figure 15B**). Though there was no correlation of the peptide ranking between the T2 HLA-A*02:01 peptide binding affinity assay and ANN in

IEDB (**Figure 15C**), the potential TAAs epitopes from MUTZ3 DCs and THP1MΦ HLA I–peptidomes had binding affinities within the same range as those of clinically validated leukemia TAAs HLA-A*02:01 epitopes, in both methods.

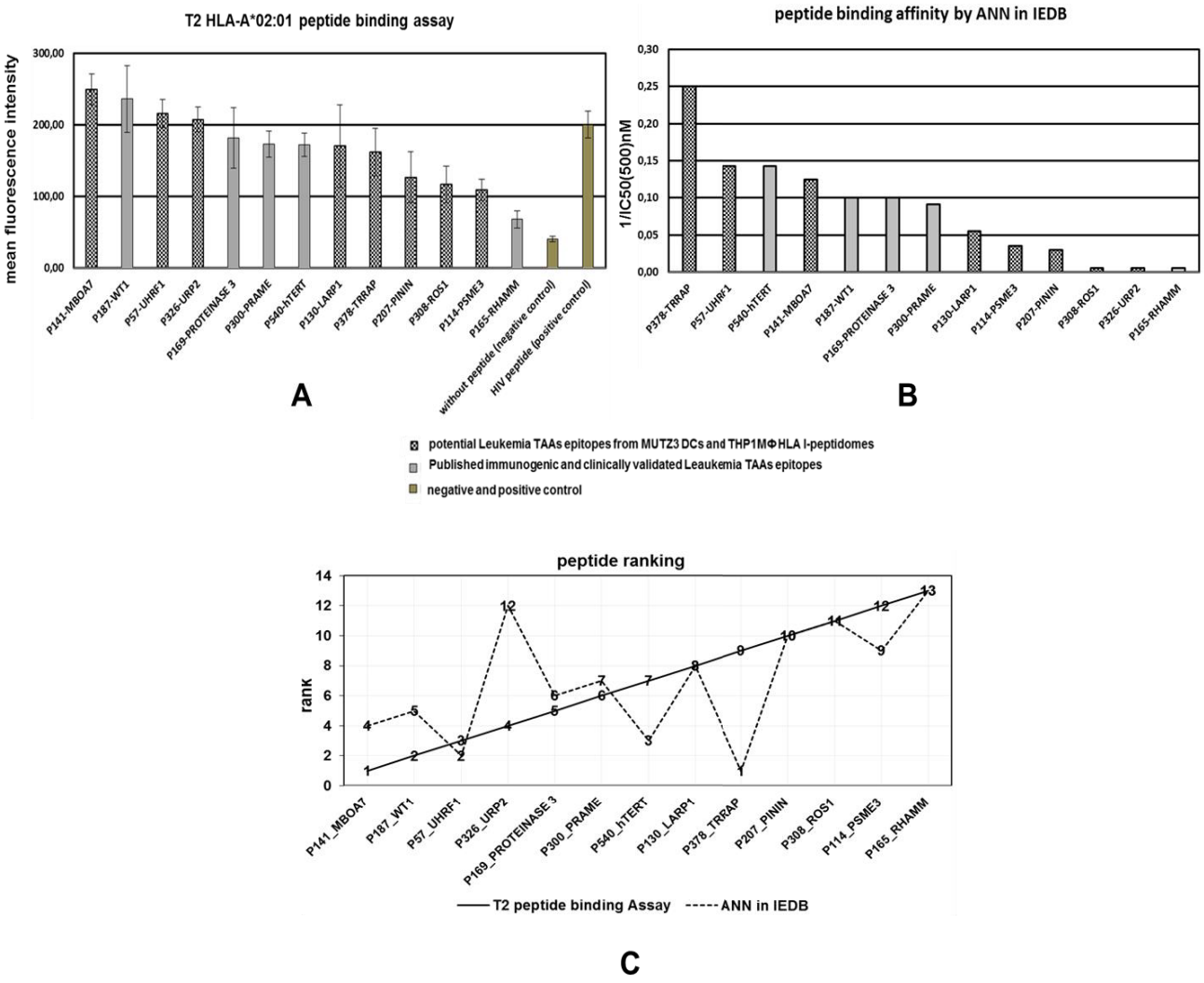


Figure 15: Peptide binding affinities and ranking based on A) T2 Cell line HLA-A2 binding assay **B)** ANN in IEDB **C)** Correlation in peptide ranking among of peptides based on T2 Cell line HLA-A2 binding assay and ANN in IEDB.

Further validation of the potential leukemia TAAs epitopes was carried out using the human INF-γ ELISpot. Peptide specific T cell responses of peptides identified from potential TAAs from THP1MΦ and MUTZ3 DCs HLA-I peptidomes **(Table 1)** and those from published

immunogenic and clinically validated leukemia TAAs HLA-A*02:01 epitopes **(Table 2)** were determined and compared. PBMCs from 4 HLA-A*02:01 positive healthy donors were stimulated for 7 days with individual peptides with addition of IL-2 at day 1 and 3, and thereafter human INFγ ELISpot analysis was carried out. The T-cell responses based on Spots Forming Units (SFU) per 1 x 10^6 PBMCS from 4 healthy donors in the ELISpot assay was in the order; P165-RHAMM > P169-PROTEINASE 3>P378-TRRAP> P308-ROS1> P187-WT1> P114-PSME3> P57-UHRF1 >P300-PRAME> P141-MBOA7> P540-hTERT> P130-LARP1>P326-URP2>P207-PININ, with spots forming units (SFU) per 1 x 10^6 PBMCS values of 262.5, 216.25, 186.25, 175, 166.25, 150, 136.25, 107.5, 102.5,100, 57.5, 37.5 and 33.75 respectively **(Figure 16).**

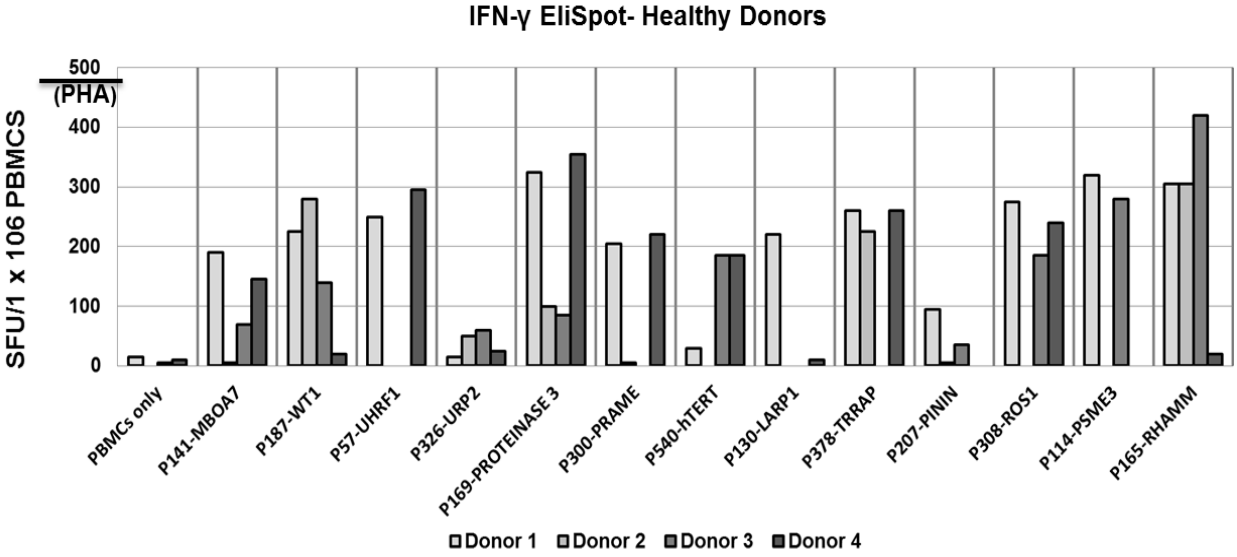


Figure 16. IFN-γ ELISPOT assay of healthy PBMCs after stimulation with published immunogenic and clinically validated leukemia TAAs HLA-A*02:01 epitopes (P540_hTERT, P300_PRAME, P187_WT1, P165_RHAMM and P169_PROTEINASE 3) and HLA-A*02:01 epitopes; P141_MBOA7 from MUTZ3 iDC, P130_LARP1 and P378_TRRAP from MUTZ3 mDC and P207_PININ, P308_ROS1, P114_PSME3, P326_URP2 and P57_UHRF1 from THP1MΦ HLA class I peptidomes derived from source proteins linked to some solid and other hematological malignancies. PHA served as a positive control and PBMCs without peptides as a negative control.

3.8 Parasite uptake and effects on viability, activation and HLA expression in THP1MΦ

To assess the uptake of LD by THP1MΦ and to determine its effects on viability and expression of HLA-ABC, HLA-A*02:01, HLA-DR and CD83 by the host, flow cytometry was used as detailed in Materials and Methods. The uptake of YFP-BHU5, a LD line transfected with the gene for YFP, by THP1MΦ based on CD11b expression versus the YFP fluorescence was 70.25±5.59%. The viability of infected THP1MΦ (THP1MΦi) was about 22% lower compared to THP1MΦ based on calcein and PI fluorescence **(Figure 17A)**. The levels of HLA-ABC (*$p<0.05$), HLA-DR and HLA-A*02:01 were lower on the infected compared to the none-infected cells, while those of macrophage activation marker CD83 were unchanged **(Figure 17B and C)**. The decrease in MHC class I and II expression in the infected cells has also been observed previously, albeit in murine studies (168).

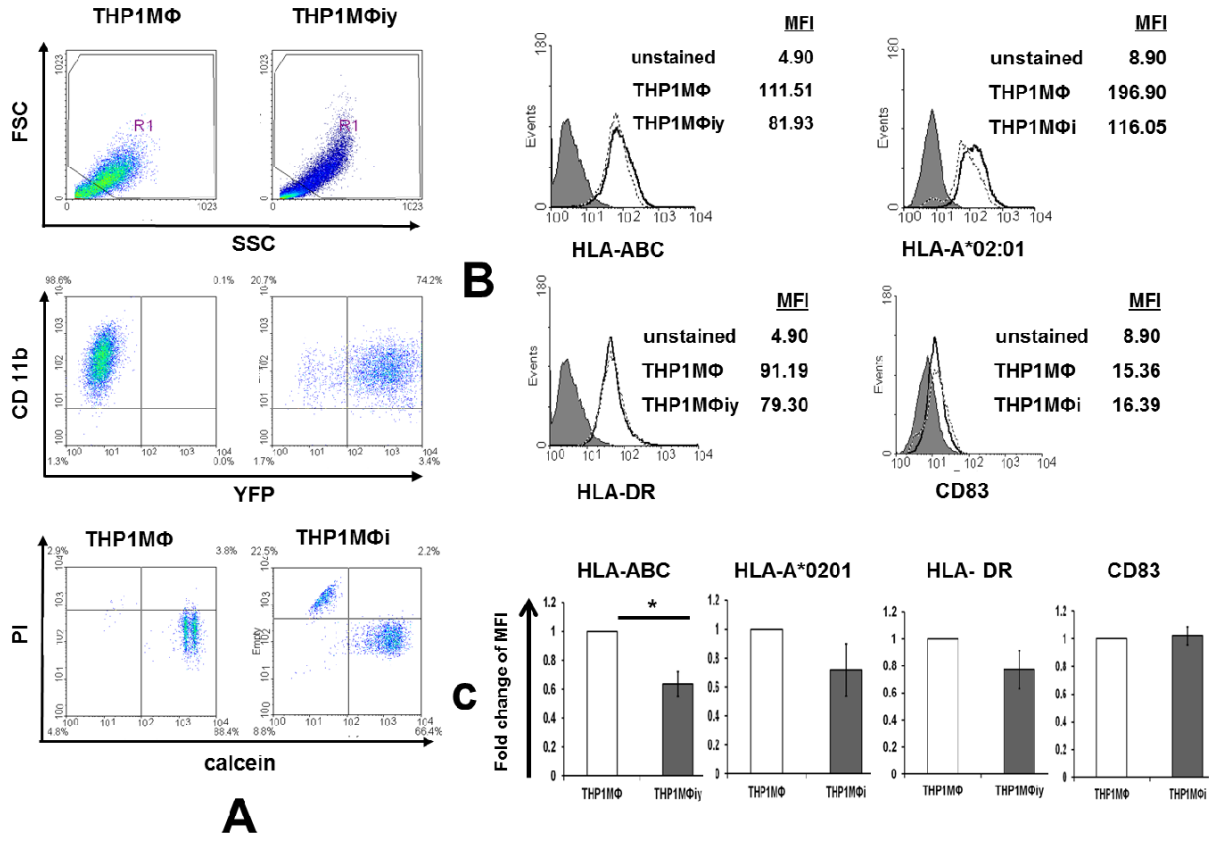


Figure 17. **Uptake of *Leishmania donovani* by THP1MΦ: effects on viability, and HLA-ABC, HLA-A*02:01, HLA-DR and CD83 expression. A)** Flow cytometric analysis of the uptake of YFP-BHU5 by THP1MΦ assessed by the YFP fluorescence in CD11b expressing THP1MΦi compared to THP1MΦ, and viability of THP1MΦ and THP1MΦi analyzed by calcein and PI staining. **B)** Expression levels of HLA-ABC, HLA-A*02:01, HLA-DR and CD83 in THP1MΦ and THP1MΦi/or THP1MΦiy. **C)** Representation of the expression levels of HLA-ABC, HLA-A*02:01, HLA-DR and CD83 as fold change of MFI in THP1Mϕi or THP1Mϕiy below/above that of THP1Mϕ. Error bars represent ±SD of the mean of three independent experiments; *$p < 0.05$ comparing THP1MΦ vs THP1MΦi or THP1MΦiy. Figure 1A and 1B are representatives of three independent experiments.

3.9 Impact of parasite uptake on constitutive and immunoproteasome mRNA expression in THP1MΦ

To determine the impact of LD on the hosts constitutive and immunoproteasome subunits expression by THP1MΦ, semi-quantitative RT-PCR was carried out as detailed in Materials and Methods. THP1MΦ and THP1MΦi expressed both the constitutive proteasome subunits (β1, β2 and β5) and the immune-proteasome subunits (βi1, βi2 and βi5) **(Figure 18A)**. Semi-

qualitative analysis of the RT-PCR bands showed a reduction of the mRNA (subunit/GADPH) of β1 (*p<0.05), β2 (*p<0.05), and with less significance β2i (p=0.28) and β5i (p=0.15) subunits in THP1MΦi compared to THP1MΦ by 14%, 25%, 9% and 25%, respectively **(Figure 18B)**.

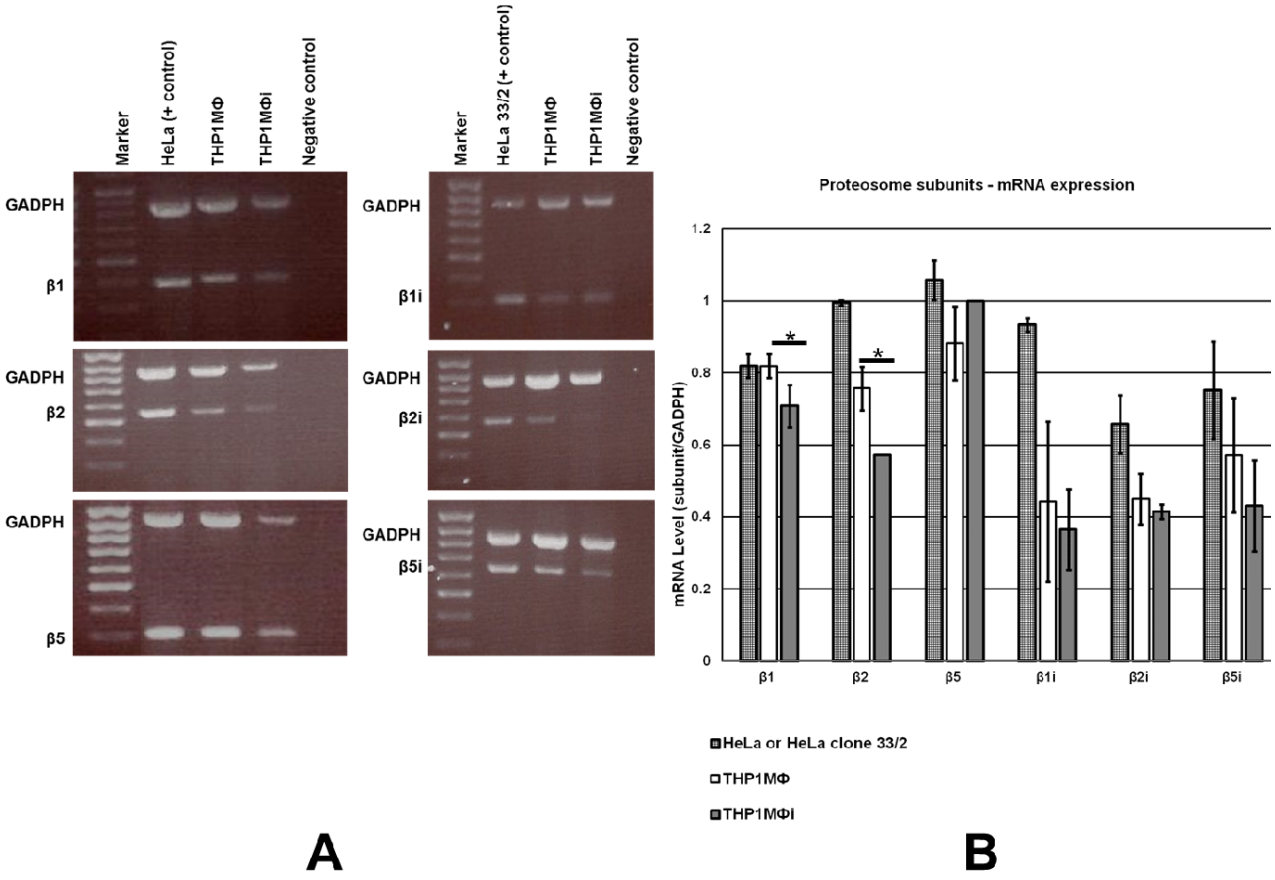


Figure 18: **mRNA expression levels of constitutive proteasome subunits β1, β2 and β5 and the immunoproteasome subunits βi1, βi2 and βi5 in THP1MΦ and THP1MΦi. A)** Agarose gel electrophoresis of RT-PCR of the proteasome subunits β1 (399bp), β2 (558bp) and β5 (275bp) and the immunoproteasome subunits βi1 (313bp), βi2 (571bp) and βi5 (648bp) in THP1MΦ and THP1MΦi, HeLa (positive control for constitutive proteasome subunits) and HeLa clone 33/2 (positive control for immunoproteasome subunits), and GADPH as internal control. **B)** Shows mean ± SD of three independent experiments of semi-quantified mRNA expression of proteasome subunits normalized to GADPH mRNA expression in the same reaction using GelAnalyser 2010. *p < 0.05 comparing THP1MΦ vs THP1MΦi.

3.10 Self-ligands presented by HLA I of THP1MΦ and THP1MΦi

2.3 x 10^9 THP1MΦi cells were lysed, and affinity chromatography and LC-MS/MS was used to isolate the HLA class I molecules and analyze the HLA-bound peptides. A total of 86 non-redundant HLA class I self-ligands were identified from 82 source proteins of THP1MΦi compared to 347 non-redundant HLA-I self-ligands derived from 282 source proteins identified for 2.8 x 10^9 THP1MΦ cells **(Supplementary table I)**. Only 17 HLA-I self-peptides sequences and 18 source proteins were found to be shared between THP1MΦ and THP1MΦi.

3.11 HLA I-bound peptide lengths in THP1MΦ and THP1MΦi

The HLA I-bound peptides were nonapeptides (55%, 59%), decapeptides (12%, 13%), octapeptides (7%, 8%), undecapetides (7%, 3%) and duodecapeptides (3%, 5%) in THP1MΦ and THP1MΦi respectively **(Figure 19)**. Thus, in both THP1MΦ and THP1MΦi the HLA I-bound peptides were dominated by nonapeptides, though the percentage in THP1MΦi was slightly higher by 4%. Nonapeptides are the optimum lengths of HLA I-bound peptides (117,164-166). The slight increase of nonapeptides in THP1MΦi compared to THP1MΦ could suggest a shift in antigen processing towards the more optimum peptide lengths for MHC I binding. With 82%, nonapeptides were also the most dominant among the peptides shared between THP1MΦ and THP1MΦi.

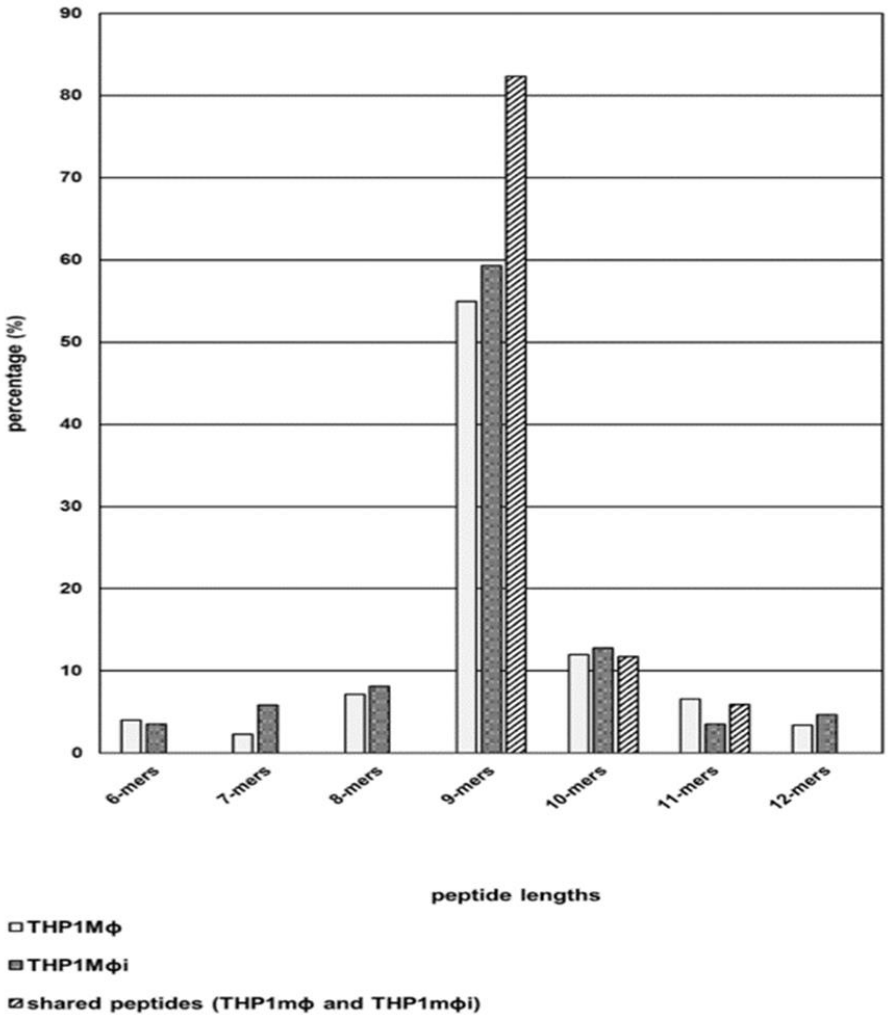


Figure 19: HLA Class I peptide lengths in THP1MΦ and THP1MΦi.

3.12 HLA assignment and binding affinities of HLA-peptides derived from THP1MΦ and THP1MΦi

The HLA restriction of the peptides was assigned using the netMHCpan in the IEDB and the canonical peptide-binding motifs in the SYFPEITHI database (120). In THP1MΦ the percentage of the peptides identified were in the order HLA-A*02:01 > HLA-B*15:11 > HLA-C*03:03 > unassigned with 35%, 33%, 19% and 13% while in THP1MΦi were in the order HLA-B*15:11 > HLA-C*03:03 > HLA-A*02:01 > unassigned with 52%, 20%, 17% and 10%, respectively **(Figure 20A)**. Thus, post infection the percentages of HLA-A*02:01-bound peptides decreased by 18% while those of HLA-B*15:11 increased by 19%; those of HLA-

C*03:03 were unaffected. For the HLA I-bound peptides shared between THP1MΦ and THP1MΦi the percentages were in the order HLA-B*15:11 > HLA-A*02:01 > HLA-C*03:03 with 71%, 18% and 12%, respectively. Binding affinity IC_{50} threshold of 500nM has been correlated to immunogenicity (167). We applied this threshold using the netMHCpan to determine the percentage HLA I peptides (8-14mers) that could stimulate CD8 T cells. The percentages of peptides within this threshold were HLA-A*02:01 (52%, 53%), HLA-B*15:11 (26%, 27%) and HLA-C*03:03 (29%, 47%) in THP1MΦ and THP1MΦi, respectively **(Figure 20B)**. The percentage of HLA-B*15:11 and HLA-A*02:01 peptides that had immune relevance in THP1MΦ and THP1MΦi was approximately the same, despite 19% increase in HLA-B*15:11- and 18% decrease in HLA-A*02:01-bound peptides identified in the infected cells. For HLA-C*03:03, the percentage of peptides that had immune relevance was higher in THP1MΦi (47%) compared to THP1MΦ (29%), though the total percentage of HLA-C*03:03 peptides identified in THP1MΦi and THP1MΦ was about the same. In addition, at IC_{50} threshold of 500nM the cumulative percentage frequencies HLA-bound peptides were dissimilar, between THP1MΦ and THP1MΦi (**Figure 20C).**

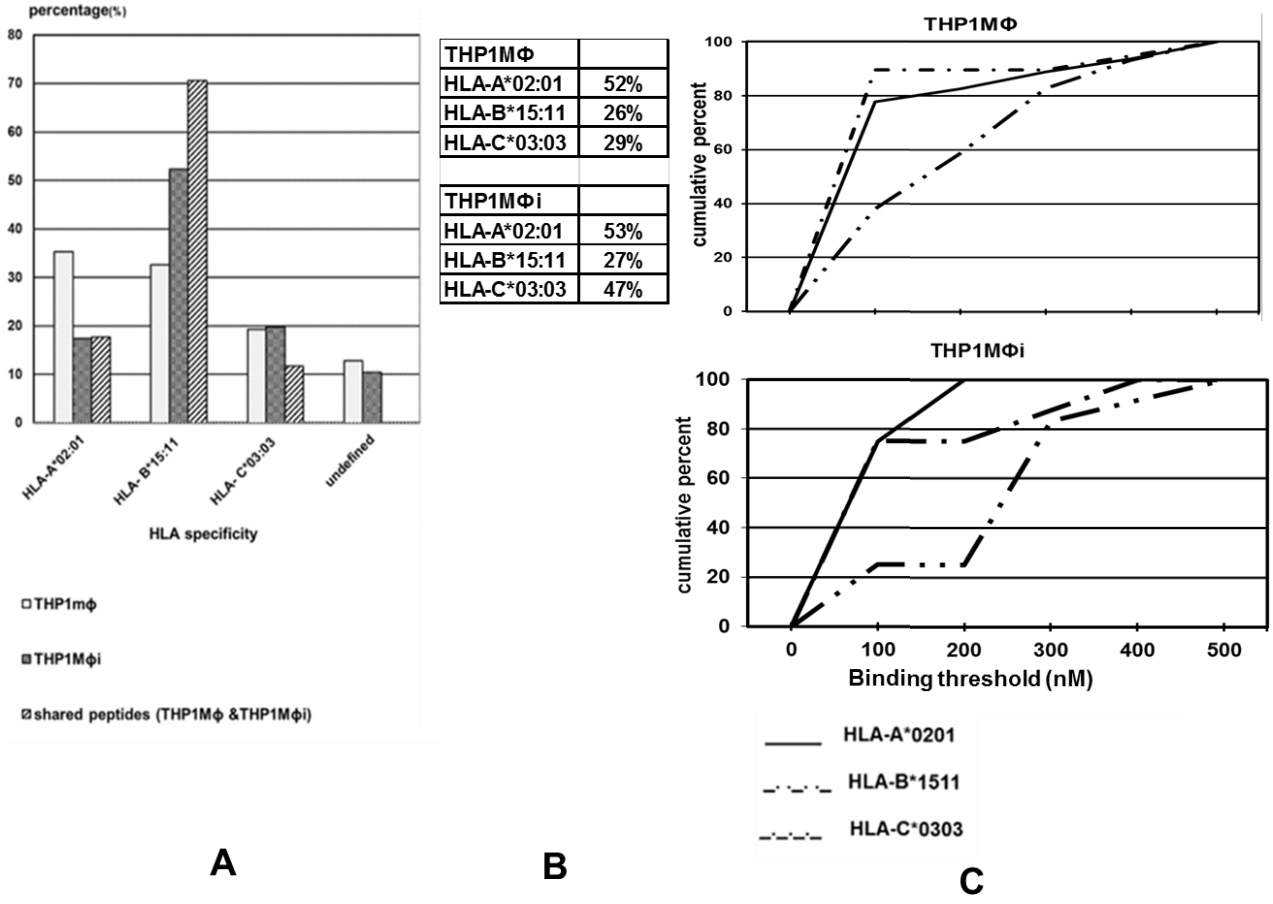


Figure 20: HLA class I self-peptide HLA restriction and binding affinities. A) MHC restriction of HLA I-bound self-peptides from THP1MΦ and THP1MΦi assigned to HLA I alleles using the canonical binding motifs according to netMHCpan in IEDB and SYFPEITHI. **C)** Percentage of THP1MΦ and THP1MΦi HLA peptides with an $IC_{50} \leq 500$nM. **B)** Cumulative percentage of THP1MΦ and THP1MΦi HLA self-peptides within an IC_{50} threshold of 500 nM.

3.13 The binding motifs for HLA I in THP1MΦ and THP1MΦi

To determine whether there was a difference in binding motifs of the nonapeptides in THP1MΦ and THP1MΦi, we used sequence logos (123,124). The most frequent primary anchor amino acids at position 2 of infected and non-infected THP1MΦ HLA-A*02:01-bound peptides were L, and with about equal but lower representation I, Y and M; for the C-terminus these were L and V. For HLA-B*15:11-bound peptides from infected and non-infected cells, P was most prominent at position 2, and Y and F at the C-terminus followed by M in case of the infected

cells. For HLA-C*03:03, A and Y were dominant at position 2 of peptides derived from non-infected cells whereas no prominence was found at this position for peptides from infected cells. At the C-terminus of HLA-C*03:03-bound peptides, L was most frequent followed by F in non-infected and M in infected THP1MΦ **(Figure 21)**.

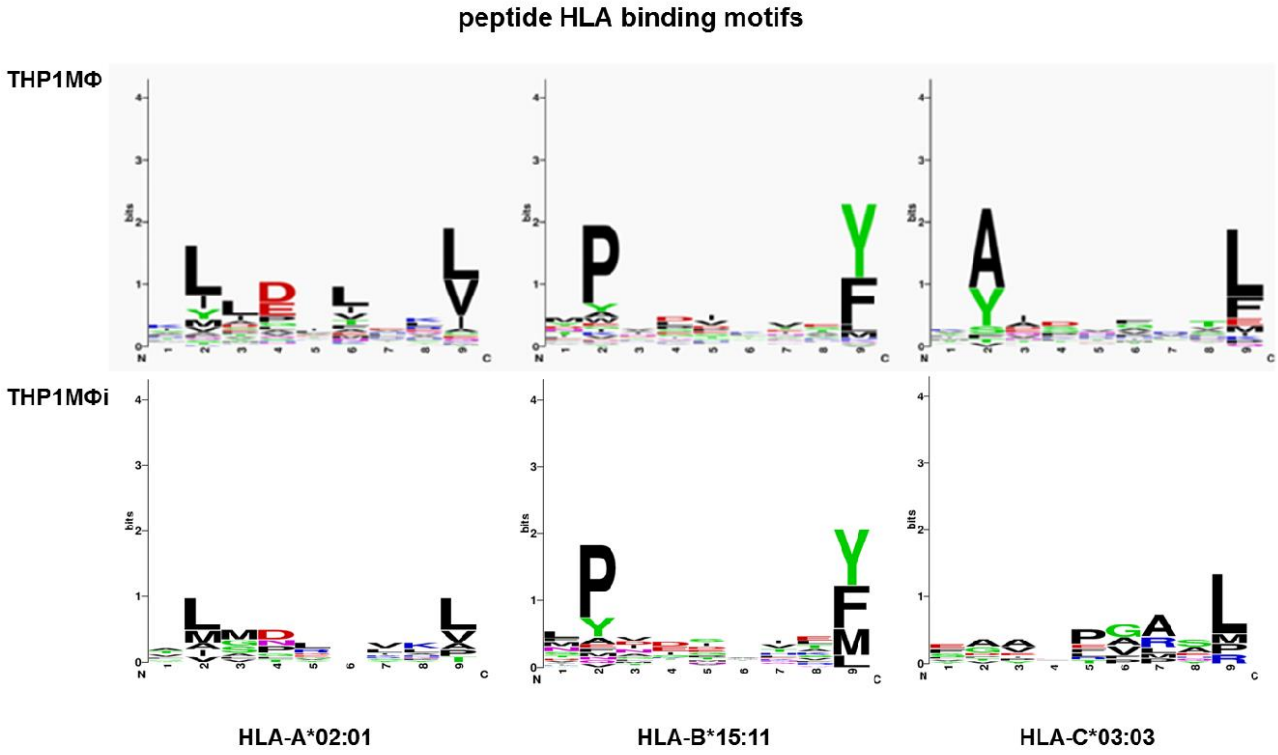


Figure 21: Binding motifs for HLA I-bound self-peptides in THP1MΦ and THP1MΦi. Sequence logos displaying the amino acid preferences for HLA-A*02:01-, HLA-B*15:11- and HLA-C*03:03-bound nonapeptides from THP1MΦ and THP1MΦi.

3.14 Subcellular locations and biological functions of source proteins in THP1MΦ and THP1MΦi

The source proteins of the HLA I-bound peptides from THP1MΦ and THP1MΦi were assigned to the respective subcellular locations and biological functions using the human protein reference database (119). The subcellular location of the source proteins from THP1MΦ and THP1MΦi were nucleus (34%, 21%), cytoplasm (23%, 16%), plasma membrane (9%, 21%),

membrane (8%, 9%), endoplasmic reticulum (6%, 3%), mitochondrion (3%, 2%), extracellular (1%, 8%), endosomes (1%, 1%), and Golgi apparatus (1%, 2%), respectively. For 5% and 14% the subcellular locations were unknown **(Figure 22A)**. In the infected cells, there was thus an increase of source proteins from plasma membrane and extracellular proteins by 12% and 7%, and a decrease in source proteins from nucleus and cytoplasm by 13% and 7%, respectively. In addition, no peptides were identified from source proteins from ribosomes, cytoskeleton and centrosome. The source proteins shared between THP1MΦ and THP1MΦi were 23% of the total source proteins in THP1MΦi and 6% of the total source in THP1MΦ and were from almost all subcellular locations in the cell.

The biological functions of the source proteins in THP1MΦ and THP1MΦi were cell communication/signal transduction (16%, 20%), protein metabolism (21%, 8%), transcription/transcription regulation (10%, 9%), transport (7%, 8%), metabolism/energy pathways (5%, 8%), cell growth and/or maintenance (10%, 8%), RNA binding (7%, 2%), immune response (3%, 9%), and DNA binding (3%, 3%). 7% and 16% of the source proteins had no known biological functions **(Figure 22B).** Post infection the percentage of source proteins involved in immune response, cell communication/signal transduction and metabolism/energy pathways increased by 6%, 4% and 3%, while those involved in protein metabolism, RNA binding, cell growth and/or maintenance decreased by 13%, 5% and 2%, respectively. The source proteins shared between THP1MΦ and THP1MΦi were mostly involved in cell communications/signal transduction (25%) and protein metabolism (15%).

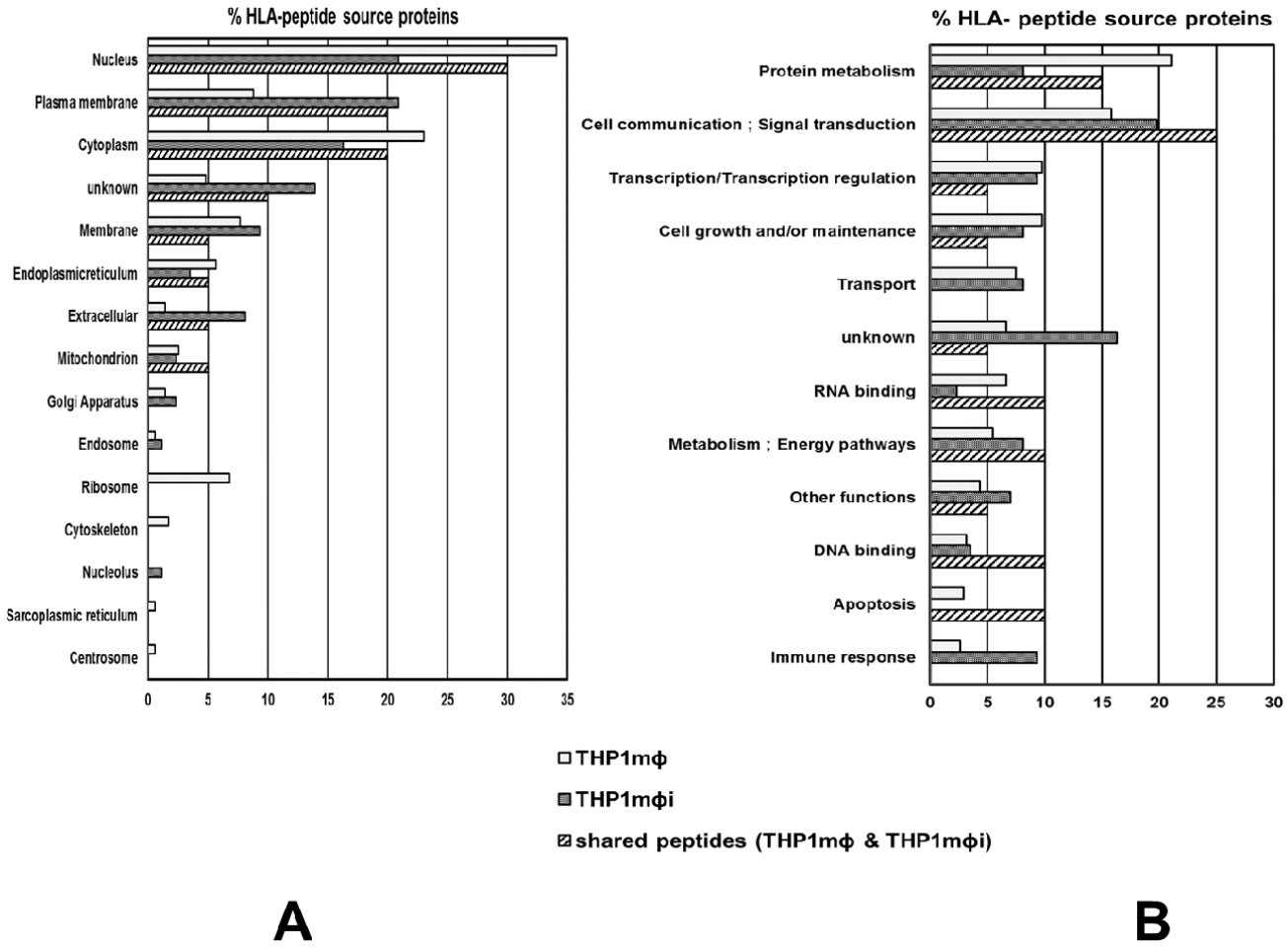


Figure 22. Subcellular locations, biological and molecular functions of the source proteins of the HLA ligands. The subcellular locations, biological and molecular functions of the source proteins of the HLA class I-bound peptides identified by mass spectrometry from THP1MΦ and THP1MΦi assigned using the Human Protein Reference Database. **A)** The subcellular locations. **B)** The biological and molecular functions.

3.15 TAAs epitopes in THP1MΦ and THP1MΦi

The HLA-A*02:01 epitopes P207_PININ, P308_ROS1, P114_PSME3, P326_URP2 and P57_UHRF1 derived from THP1MΦ HLA class I–peptidomes **(Table 3),** that were shown to be comparatively good to the published immunogenic and clinically validated leukemia TAAs HLA-A*02:01 epitopes **(Table 2)** in reference to their HLA binding affinities and ability to stimulate CD8 + T cell responses **(Figure 15, and 16)**; were not identified in THP1Mϕi HLA-class I peptidome based on peptide sequences, and precursor peptide mass signals and retention time.

4. Discussion

The total number of HLA class I restricted peptides and source proteins identified in MUTZ3 DCs and THP1MΦ was about the same, and they were heterogeneous and individualized, despite the MUTZ3 iDCs and mDCs expressing the same HLA alleles, and sharing one common with THP1MΦ. Only a small fraction of HLA I peptides and source proteins were found to be shared between the MUTZ3 DCs, and among the MUTZ3 DCs and the THP1MΦ. The heterogeneity and individualization was slightly higher for the HLA peptides than for the source proteins, as the number of shared source proteins were slightly higher compared to those of the HLA I peptides. This has been observed also in other human cell lines and tumor samples (117,164,166), and depicts differences in the antigen processing and presentation in the two variant MUTZ3 DC differentiation states, and THPMΦ.

Despite the fact that the HLA peptides and the source proteins were heterogeneous and individualized, a number of similarities were observed in the HLA peptidomes and the source proteins. Firstly, in MUTZ3 DCs and THP1MΦ nanopeptides were the most dominant, and constituted 50% of all the identified peptides, followed by decapeptides with approximately 25% of peptides in MUTZ3 DCs, compared to 12% in THP1MΦ. Secondly, in both MUTZ3 DCs, the percentage of peptides identified by LC-MS/MS declined in the order HLA-B44 ≥ HLA-A*02:01 ≥ HLA-A3 ≥ HLA-B56 and the specific HLA peptides had similar dominant anchor residues at position 2 and the C-terminus with only minor differences in the order and identity. This similarity in the anchor motifs was also observed in HLA-A*02:01-bound peptides from MUTZ3 DCs and THP1MΦ. The numbers of HLA-B56 peptides were low for any conclusive comparison in the anchor motifs. Thirdly, in both MUTZ3 DC phenotypes, the HLA-A*02:01-associated peptides were stronger HLA binders followed by HLA-B44, HLA-A3, and lastly HLA-B56. For HLA-B56 no peptides were predicted for the IC_{50} (500) nM threshold, suggesting that HLA-B56-associated peptides are low affinity binders (169).

Similarities were also observed in MUTZ3 DCs and THP1MΦ subcellular locations and molecular functions of HLA-I peptides source proteins. Firstly, the source proteins were derived from almost all subcellular locations with nucleus, cytoplasm, plasma membrane and the endoplasmic reticulum being the most dominant **(Figure 17),** which is similar for the HLA peptidome of melanoma tumor samples (117,164) but different for other human samples such as the B-lymphoblastoid cell line, where no source proteins from plasma membrane were found, (165) and multiple sclerosis autopsy samples where cytoplasm and plasma membrane were the most dominant, 34% and 24%, respectively (166). Secondly, the source proteins were involved in various molecular functions but especially in cell communication/signal transduction, protein metabolism, and transcription factor activity/regulator activity, and the proportion of source proteins per molecular function was similar. In contrast, in the B lymphoblastic cell line 721.221, the source proteins were dominantly involved in declining prominence in metabolism, cell growth and/or maintenance, cell communication, and stress response (165), and in multiple sclerosis autopsy samples, they were dominantly involved in cellular assembly and organization, nervous system development and function, cellular growth and proliferation (166). The similarities in source protein peptide sampling in MUTZ3 DCs and THP1MΦ, though unconfirmed, would imply similarities in protein turnover, as protein turnover correlates with source protein peptide sampling (170,171).

In reference to Leukemia TAAs MUTZ3 DCs and THP1MΦ were able to sample peptides from different potential Leukemia TAAs **(Table 3),** and these peptides were as good as the published immunogenic and clinically validated Leukemia TAAs epitopes in Table 2, in terms of MHC-peptide binding affinities and ability to stimulate CD8+ T cells **(Figure 15 A and B).** The heterogeneity in TAAs peptide sampling would be due to differences in the antigen processing and presentation in the two variant MUTZ3 DC differentiation states, and THPMΦ, and due to

specific differences in TAAs protein expression and turnover (unconfirmed), as protein turnover also correlates with source protein peptide sampling (170,171).

The antigen processing and presentation in MUTZ3 DCs and THP1MΦ was different considering the low degree of overlap in the HLA I-bound peptides, but similaraties in source peptide sampling in the shared proteins would imply similarities in protein turnover. Further evaluation of the HLA peptidome in the presence of a pathogen was vital to fully understand the antigen processing and presentation of self and, hence, on the immunogenicity of the cells, and the specificities of the resulting T cell responses. In this regard, THP1MΦ (primary host) was infected with LD.

Upon infecting THP1MΦ with LD, the total number of HLA class I-restricted self-peptides and source proteins identified from THP1MΦi was four-fold lower compared to those identified in THP1MΦ, and were heterogeneous and individualized. Only a few peptides were found to be shared between the two despite expressing the same HLA alleles.

The strong decrease in the number of HLA class I-restricted peptides from LD-infected THP1MΦ has been reproduced in independent experiments but no single cause could be identified; rather, it might be due to cumulative effects. Firstly, the overall MHC-I expression at the cell surface of THP1MΦi was lower compared to THP1MΦ, including that of HLA-A*02:01 though not significant **(Figure 17B and C)**. Reduction of MHC I-restricted antigen presentation upon infection with LD parasites through reduction of MHC I present at the cell surface has also been observed in murine studies albeit no comparative peptidome studies were done (168). Though our focus was on HLA I-restricted self-peptides, we also observed lower expression of MHC-II in THP1MΦi compared to THP1MΦ. This observation concurred with murine and human studies on MHC-II, and showed that *Leishmania* inhibits antigen

presentation by repressing MHC-II expression (168,172,173). Secondly, the infection of THP1MΦ by LD resulted in about 22% decrease in host cell viability **(Figure 17A**), which might be due to the fact that naturally *Leishmania* promastigotes, upon uptake by macrophages, transform to amastigotes and multiply to eventually rapture the macrophages (174). Thirdly, although CD83 expression, a marker of macrophage activation, was basically unchanged in THP1MΦi compared to THP1MΦ indicating a lack of activation, the LD infection resulted in decreased expression of both constitutive (β1 and β2) and immunoproteasome (β2i and β5i) subunits, which could translate into decreased antigen processing efficiency. The impact of immunoproteasome on the quality and quantity of MHC class I ligands had been studied using wild type and $\beta2i^{-/-}/\beta5i^{-/-}$-double deficient murine dendritic cells (175) and $\beta1i^{-/-}/\beta2i^{-/-}/\beta5i^{-/-}$-triple deficient murine spleen cells (176): where increased expression of immunoproteasome subunits correlated with increased generation of peptides that are suitable for binding to MHC I molecules.

The heterogeneity and individuality in the HLA-I self-peptides and source proteins identified in THP1MΦ and THP1MΦi depicts differences in protein expression and turnover, and processing and presentation, as was in other cells and tumor samples (117,164,166). The nonapeptides are the optimum lengths for MHC class I binding, and though the infection of THP1MΦ by LD did not change the nonapeptides dominance in the identified HLA I-bound peptides, profound differences in antigen processing and presentation were evident, firstly, in the HLA restriction of identified peptides. For THP1MΦ the percentage of the peptides identified for the different HLA-restrictions ranked in the order HLA-A*02:01 > HLA-B*15:11 > HLA-C*03:03 while in THP1MΦi they were in the order HLA-B*15:11 > HLA-C*03:03 > HLA-A*02:01. Though HLA-B*15:11 peptides were dominant after infection with LD, only 26% of them were within the IC_{50} threshold of 500nM. In general, after infection there was a shift of peptides towards lower affinity binders. A previous systematic mapping and

characterizing of peptide ligands derived from B*1508, B*1501, B*1503, and B*1510 showed endogenous peptide loaded into B15 to be flexible both in the location of and amino acids at the N-proximal anchors (177). In addition to this, additional preference of aliphatic amino acids was observed at the C-Terminus after infection which would, though unconfirmed in Prilliman et al, 1999, result in lower binding affinity of the peptides. The differences in antigen processing and presentation were evident in the peptide anchor motifs. For the HLA-A*02:01-bound peptides there were no dominant accessory anchor amino acids at position 6 in THP1MΦi compared to the dominant hydrophobic anchor in THP1MΦ. For HLA-C*03:03 there was no anchor motifs at position 2 in THP1MΦi but a strong preference for A and Y in THP1MΦ but a higher percentage of peptides within the IC_{50} threshold of 500nM in THP1MΦi compared to THP1MΦ.

In both THP1MΦ and THP1MΦi the peptide source proteins were derived from almost all subcellular locations and were involved in almost all molecular functions of the cells. But differences were observed. Firstly, in THP1MΦi compared to THP1MΦ, there was an increase of source proteins from plasma membrane and extracellular proteins and a decrease in source proteins from nucleus and cytoplasm **(Figure 22A),** and no peptides were identified from ribosomes, cytoskeleton and centrosomes unlike in THP1MΦ. Secondly, in THP1MΦi compared to THP1MΦ, there was an increase of source proteins involved in immune responses, cell communication/signal transduction and metabolism/energy pathways, a decrease in those involved in protein metabolism, RNA binding, cell growth and/or maintenance (**Figure 22B**), and non sampling of potential Leukemia TAAs in Table 3. The differences in source protein peptide sampling in THP1MΦ and THP1MΦi would imply differences in protein turnover, as protein turnover correlates with source protein presentation (170,171).

The infection of macrophages with LD has profound effects on the self-peptide repertoire presented by MHC I molecules which in parts can be explained with changes in antigen processing including the composition of the proteasomes, and altered protein expression and turn-over in different cellular compartments. Summarizingly, the self-displayed by infected macrophages is very different from the self of uninfected cells. The implication of this phenomenon in Leishmaniasis remains to be elucidated but may explain autoimmunity phenomena in Leishmaniasis, manifested as ulceration in the skin mucosa.

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6. Appendix

6.1 **Supplementary table 1:** HLA I ligands and source proteins identified from MUTZ3 iDC, MUTZ3mDC, THP1Mϕ and THP1Mϕi.

MUTZ3 iDC

No.	Peptide sequence	Source protein	Observed Mass[M+H]+	Mascot Score	HLA	Subcellular localisation	Biological function
1	FIGYPITL	Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens GN=HSP90AB3P PE=5 SV=1 H90B3_HUMAN	922,51	33	A2.1	Cytoplasm	protein folding
2	ILYGKIIHL	Chromosome transmission fidelity protein 8 homolog OS=Homo sapiens GN=CHTF8 PE=1 SV=1 CTF8_HUMAN	1068,66	39	A2.1	Nucleus	Signal transduction ; Cell communication
3	TLADLVHHV	Transformation/transcription domain-associated protein OS=Homo sapiens GN=TRRAP PE=1 SV=3 TRRAP_HUMAN	1003,54	53	A2.1	Nucleus	Transcription/Transcription regulation
4	HVPEHAVVL	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 FAS_HUMAN	999,56	54	A2.1	Cytoplasm	Metabolism ; Energy pathways
5	ALSNLEVKL	Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1 URP2_HUMAN	985,57	50	A2.1	Plasma membrane	unknown
6	GLLPDVPSL	Lysophospholipid acyltransferase 7 OS=Homo sapiens GN=MBOAT7 PE=1 SV=2 MBOA7_HUMAN	909,51	28	A2.1	Plasma membrane	Metabolism ; Energy pathways
7	GLIDHQTYL	Plectin GN= PLEC PLEC_HUMAN	1058.5397	15	A2.1	Cytoskeleton	unknown
8	SLIKQIPRI	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 RL10A_HUMAN	1066,68	38	A2.1	Ribosome	protein metabolism
9	VFDPVPVGV	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 DHX9_HUMAN	927,5	31	A2.1	Nucleus	Transcription/Transcription regulation

10	SIAEGRISL	BUTYROPHILIN-LIKE PROTEIN 8 OS=HOMO SAPIENS GN=BTNL8 PE=1 SV=1 BTNL8_HUMAN	944,52	49	A2.1	membrane	Immune response
11	NLLPKLHIV	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 CLIC1_HUMAN	1045,66	22	A2.1	Nucleus	Transport
12	YYDGKMVQL	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 TOP1_HUMAN	1115,54	13	A2.1	Nucleus	DNA topoisomerase activity
13	LLIENVASL	Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 PE=1 SV=4 GPX1_HUMAN	970,56	26	A2.1	Cytosol	Anti-apoptosis
14	YLTAEILEL	Histone H2A type 1-A OS=Homo sapiens GN=HIST1H2AA PE=1 SV=3 H2A1A_HUMAN	1063,57	27	A2.1	Nucleus	DNA binding
15	VMAPRTLLL	HLA class I histocompatibility antigen, A-1 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 1A01_HUMAN	1012,6	29	A2.1	Plasma membrane	Immune response
16	VLSSRLAFA	HLA class II histocompatibility antigen, DR beta 3 chain OS=Homo sapiens GN=HLA-DRB3 PE=1 SV=1 DRB3_HUMAN	962,55	41	A2.1	Plasma membrane	Immune response
17	KRGDVIYIL	Src kinase-associated phosphoprotein 2 OS=Homo sapiens GN=SKAP2 PE=1 SV=1 SKAP2_HUMAN	1075,63	42	A2.1	Cytoplasm	Cell communication ; Signal transduction
18	SLAEGLRTV	2'-5'-oligoadenylate synthase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=3 OAS3_HUMAN	944,52	67	A2.1	Cytoplasm	Immune response
19	ILMEHIHKL	60S ribosomal protein L19 RL19_HUMAN	1132.6427	56	A2.1	Ribosome	Protein metabolism
20	ALADIAVGV	Adenosine receptor A3 OS=Homo sapiens GN=ADORA3 PE=2 SV=2 AA3R_HUMAN	827,46	55	A2.1	Plasma membrane	Cell communication ; Signal transduction
21	TLDDLIAAV	Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 PE=1 SV=1 ANKH1_HUMAN	929,49	52	A2.1	Cytoplasm	Anti-apoptosis
22	MLFPGSIAL	APC-binding protein EB1	947,52	-	A2.1	Centrosome	Cell communication ; Signal transduction
23	ALADGVQKV	Apolipoprotein L1 OS=Homo sapiens GN=APOL1 PE=1 SV=5 APOL1_HUMAN	899,49	60	A2.1	Extracellular	Transport ; Lipid metabolism
24	YLKDLIEEV	Cyclic AMP-dependent transcription factor ATF-4 GN=ATF4 ATF4_HUMAN	1120,59	-	A2.1	Nucleus	Transcription regulation

25	YLDNGVVFV	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1 DDB1_HUMAN	1024,53	13	A2.1	Cytoplasm	DNA repair
26	HLANIVERV	E3 ubiquitin-protein ligase TRIM22 TRI22_HUMAN	1049.5982	13	A2.1	Cytoplasm	Transcription/Transcription regulation
27	ALHHAVIFL	Endoplasmic reticulum metallopeptidase 1 OS=Homo sapiens GN=ERMP1 PE=1 SV=2	1019,58	42	A2.1	Membrane	unknown
28	SLYDYNPNL	Eukaryotic translation initiation factor 3 subunit C EIF3C_HUMAN	1097.5029	21	A2.1	Cytoplasm	Protein metabolism
29	SLASLLVSV	Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3 EXOS7_HUMAN	887,54	61	A2.1	Nucleolus	Ribonuclease activity
30	ALSDHHIYL	Fructose-bisphosphate aldolase A ALDOA_HUMAN	1067.5400	26	A2.1	Cytoplasm	Metabolism ; Energy pathways
31	LLDVPTAAV	Gamma-interferon-inducible lysosomal thiol reductase OS=Homo sapiens GN=IFI30 PE=1 SV=3 GILT_HUMAN	897,53	-	A2.1	Lysosome	Metabolism ; Energy pathways
32	GLMDTVKKV	Glucocorticoid modulatory element-binding protein 1 OS=Homo sapiens GN=GMEB1 PE=1 SV=2 GMEB1_HUMAN	989,53	21	A2.1	Nucleus	Transcription/Transcription regulation
33	NLAENISRV	Glycogen phosphorylase, brain form PYGB_HUMAN	1014.5458	41	A2.1	Cytoplasm	Metabolism ; Energy pathways
34	ILFGHENRV	Guanine nucleotide-binding protein subunit beta-5 GN=GNB5 GBB5_HUMAN	1083.5825	51	A2.1	Membrane fraction	Signal transduction ; Cell communication
35	SLLENLEKI	Heterogeneous nuclear ribonucleoprotein C-like 1 OS=Homo sapiens GN=HNRNPCL1 PE=1 SV=1 HNRCL_HUMAN	1057,59	37	A2.1	Nucleus	RNA binding
36	LLFDRPMHV	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 HNRPM_HUMAN	1126,59	32	A2.1	Nucleus	Ribonucleoprotein
37	RMLPHAPGV	Histone deacetylase 2 OS=Homo sapiens GN=HDAC2 PE=1 SV=2 HDAC2_HUMAN	976,52	27	A2.1	Nucleus	Transcription/Transcription regulation
38	VMAPRTLVL	HLA class I histocompatibility antigen, A-2 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1	998,59	33	A2.1	Plasma membrane	Immune response
39	MVDGTLLLL	HLA class I histocompatibility antigen, alpha chain E OS=Homo sapiens GN=HLA-E PE=1 SV=3	973,56	27	A2.1	Plasma membrane	Immune response

40	FIIQGLRSV	HLA class II histocompatibility antigen, DQ alpha 2 chain OS=Homo sapiens GN=HLA-DQA2.1 PE=2 SV=2 DQA2.1_HUMAN	1031,6	27	A2.1	Plasma membrane	Immune response
41	ILLDVKTRL	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 K1C14_HUMAN	1069,69	60	A2.1	Cytoplasm	Cell growth and/or maintenance
42	VLIPKLPQL	ORM1-like protein 3 OS=Homo sapiens GN=ORMDL3 PE=1 SV=1 ORML3_HUMAN	1019,68	59	A2.1	Endoplasmic reticulum	Protein metabolism
43	YLLDQHILI	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 OS=Homo sapiens GN=INPP5D PE=1 SV=2 SHIP1_HUMAN	1126,63	31	A2.1	Cytoplasm	Signal transduction ; Cell communication
44	LLIDHRFLL	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform OS=Homo sapiens GN=PIK3CG PE=1 SV=3	1138,69	32	A2.1	Plasma membrane	Cell communication ; Signal transduction
45	ALMDEVVKA	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 PGK1_HUMAN	974,49	42	A2.1	Cytoplasm	Metabolism ; Energy pathways
46	SLLDKIIGA	Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1 PTRF_HUMAN	928,55	55	A2.1	Nucleus	Transcription/Transcription regulation
47	YLLPAIVHI	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2	1037,64	42	A2.1	Nucleus	ATPase activity
48	QLVDIIEKV	Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 PSME3_HUMAN	1055,62	61	A2.1	Cytoplasm	Protein metabolism
49	TLWVDPYEV	Protein BTG2 OS=Homo sapiens GN=BTG2 PE=1 SV=1 BTG2_HUMAN	1120,54	31	A2.1	Nucleus	Transcription/Transcription regulation
50	FLFNKVVNL	Protein yippee-like 5 OS=Homo sapiens GN=YPEL5 PE=2 SV=1	1092,64	24	A2.1	unknown	unknown
51	ILDKKVEKV	Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens GN=HSP90AB3P PE=5 SV=1 H90B3_HUMAN	1070,66	52	A2.1	cytoplasm	protein folding
52	VFDEAIRAV	Ras-related C3 botulinum toxin substrate 1 RAC1_HUMAN	1018.5447	58	A2.1	Plasma membrane	Cell communication ; Signal transduction
53	SLVDTVYAL	Rho guanine nucleotide exchange factor 6 OS=Homo sapiens GN=ARHGEF6 PE=1 SV=2 ARHG6_HUMAN	979,51	24	A2.1	Cytoplasm	Cell communication ; Signal transduction
54	KLHGVNINV	RNA-binding protein 4B OS=Homo sapiens GN=RBM4B PE=1 SV=1 RBM4B_HUMAN	992,56	39	A2.1	Cytoplasm	RNA binding

55	SIIGRLLEV	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1	998,61	35	A2.1	Cytoskeleton	Cell proliferation
56	VLWDRTFSL	Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2 STAT1_HUMAN	1135,59	37	A2.1	Cytoplasm	Transcription/Transcription regulation
57	TLSDLRVYL	Sulfiredoxin-1 OS=Homo sapiens GN=SRXN1 PE=1 SV=2 SRXN1_HUMAN	1078,59	44	A2.1	cytoplasm	Metabolism ; Energy pathways
58	FLLDKKIGV	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 TCPB_HUMAN	1031,64	43	A2.1	Cytoplasm	Protein metabolism
59	SFDGIIAMM	Transcription elongation factor SPT4 OS=Homo sapiens GN=SUPT4H1 PE=1 SV=1	983,45	51	A2.1	Nucleus	Transcription/Transcription regulation
60	NIIELVHQV	Tyrosine-protein kinase SYK OS=Homo sapiens GN=SYK PE=1 SV=1 KSYK_HUMAN	1063,58	23	A2.1	Cytoplasm	Cell communication ; Signal transduction
61	ALLDKLYAL	U3 small nucleolar ribonucleoprotein protein IMP3 OS=Homo sapiens GN=IMP3 PE=1 SV=1 IMP3_HUMAN	1018,6	57	A2.1	Nucleus	RNA binding
62	AVSNHVFHL	Zinc finger MIZ domain-containing protein 1 OS=Homo sapiens GN=ZMIZ1 PE=1 SV=3 ZMIZ1_HUMAN	1022,54	38	A2.1	Nucleus	Transcription/Transcription regulation
63	SVALKGHSL	Zinc finger protein 518B OS=Homo sapiens GN=ZNF518B PE=2 SV=2 Z518B_HUMAN	910,51	22	A2.1	Nucleus	unknown
64	PLVSVVDTI	V-type proton ATPase subunit C 2 OS=Homo sapiens GN=ATP6V1C2 PE=2 SV=2 VATC2_HUMAN	941,54	38	A2.1	unknown	Metabolism ; Energy pathways
65	ILMEHIHKL*	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1 RL19_HUMAN	1148,62	30	A2.1	Ribosome	Protein metabolism
66	VMAPRTLVL*	HLA class I histocompatibility antigen, A-2 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 1A02_HUMAN	1014,58	28	A2.1	Plasma membrane	Immune response
67	VMAPRTLLL*	HLA class I histocompatibility antigen, A-1 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 1A01_HUMAN	1028,59	20	A2.1	Plasma membrane	Immune response
68	VFDEAIRAVL	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1 RAC1_HUMAN	1131,62	52	A2.1	Cytoplasm	Cell communication ; Signal transduction

69	SLINVGLISV	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1 AN32B_HUMAN	1013,61	57	A2.1	Nucleus	cell cycle, Anti apoptotic
70	GIFGGHIRSV	Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2 UBP10_HUMAN	1041,57	59	A2.1	Cytoplasm	Protein metabolism
71	KVCNPIITKL	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 HSP7C_HUMAN	1127,67	39	A2.1	Cytoplasm; Nucleolus	Protein metabolism
72	TIIDLPGITRV	Interferon-induced GTP-binding protein Mx2 OS=Homo sapiens GN=MX2 PE=1 SV=1 MX2_HUMAN	1196,7	42	A2.1	Nucleus	Immune response
73	RLFVGSIPK	Heterogeneous nuclear ribonucleoprotein R GN= HNRNPR HNRPR_HUMAN	1015.6178	35	A3	Nucleus	RNA binding
74	SLMHSFILK	Dynein light chain roadblock-type 1 OS=Homo sapiens GN=DYNLRB1 PE=1 SV=3 DLRB1_HUMAN	1074,59	45	A3	cytoplasm	unknown
75	LSLEMIQLK	CGMP-DEPENDENT PROTEIN KINASE 2 OS=HOMO SAPIENS GN=PRKG2 PE=1 SV=1 KGP2_HUMAN	1073,63	52	A3	Plasma membrane	Cell communication ; Signal transduction
76	KIADRFLLY	LIM domain transcription factor LMO4 OS=Homo sapiens GN=LMO4 PE=1 SV=1 LMO4_HUMAN	1137,65	39	A3	Nucleus	Transcription/Transcription regulation
77	AIYGTRKFK	Macrophage-expressed gene 1 protein OS=Homo sapiens GN=MPEG1 PE=2 SV=1 MPEG1_HUMAN	1082,61	40	A3	membrane	unknown
78	FVLPELPSV	MAPK-activating protein PM28	999,57	-	A3	Membrane	DNA binding
79	GVADKILKK	N-myc-interactor OS=Homo sapiens GN=NMI PE=1 SV=2 NMI_HUMAN	970,6	53	A3	Cytoplasm	Transcription/Transcription regulation
80	YGNTLVEFR	Olfactomedin-like protein 2B OS=Homo sapiens GN=OLFML2B PE=2 SV=2 OLM2B_HUMAN	1097,55	21	A3	Extracellular	unknown
81	ISLKQAPLVH	Clathrin light chain A CLCA_HUMAN	1104.6655	70	A3	Cytoplasm	Cell growth and/or maintenance
82	KLFDHAVSKF	Long-chain-fatty-acid--CoA ligase 4 ACSL4_HUMAN	1190.6448	66	A3	Microsome	Metabolism ; Energy pathways
83	VVLRNPLIAGK	Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1 SMD2_HUMAN	1178,75	51	A3	Nucleus	RNA binding

84	ESGPSIVHRKCF	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 ACTG_HUMAN	1358,66	61	A3	Cytoplasm	Cell growth and/or maintenance
85	TLLDIDNTRMTL	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 K1C9_HUMAN	1404,71	59	A3	Cytoplasm	Cell growth and/or maintenance
86	SVIVVLRNPLIAGK	Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1 SMD2_HUMAN	1477,93	67	A3	Nucleus	RNA binding
87	MEKIWHHTF	Actin, cytoplasmic 1 ACTB_HUMAN	1227.5859	57	B44	Cytoplasm	Cell growth and/or maintenance
88	SEHSIIKDF	DNA replication licensing factor MCM5 MCM5_HUMAN	1074.5346	43	B44	Nucleus	DNA binding
89	NEDLRKELW	E3 ISG15--protein ligase HERC5 HERC5_HUMAN	1201.6091	17	B44	Cytoplasm	Cell communication ; Signal transduction
90	EENSMRLDL	Leucine-rich repeat protein SHOC-2 GN= SHOC2 SHOC2_HUMAN	1105.5073	27	B44	Cytoplasm	Cell communication ; Signal transduction
91	QEVFEKATF	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 NUCL_HUMAN	1097.5393	45	B44	Nucleolus	RNA binding
92	EEAPVLMHY	Prostaglandin G/H synthase 1 GN= PTGS1 PGH1_HUMAN	1087.5008	47	B44	Endoplasmic reticulum	Metabolism ; Energy pathways
93	SEMDKVRVF	Protein-arginine deiminase type-4 GN=PADI4 PADI4_HUMAN	1109.5539	23	B44	Nucleus	Metabolism ; Energy pathways
94	QEWDKYCHY	Squalene synthase GN=FDFT1 FDFT_HUMAN	1270.5077	29	B44	Endoplasmic reticulum	Metabolism ; Energy pathways
95	TEVTGHRW	Basigin OS=Homo sapiens GN=BSG PE=1 SV=2 BASI_HUMAN	984,48	67	B44	Plasma membrane	Cell communication ; Signal transduction
96	REVTIPDL	Tenascin-X OS=Homo sapiens GN=TNXB PE=1 SV=3 TENX_HUMAN	941,51	23	B44	Extracellular	Cell growth and/or maintenance
97	EESYSRMGY	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2 SFPQ_HUMAN	1120,45	28	B44	Nucleus	RNA binding
98	FEYEYSQRW	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2 SFPQ_HUMAN	1306,57	51	B44	Nucleus	RNA binding
99	QESNVRLKL	Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3 SEP11_HUMAN	1085,6	34	B44	Perinuclear region	Cell cycle ; Vesicle-mediated transport
100	QEEPGKGSFW	Forkhead box protein K1 FOXK1_HUMAN	1163.5247	36	B44	Nucleus	Transcription/Transcription regulation

101	AEIEIMKKL	Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2 PE=1 SV=2 IF2B2_HUMAN	1073,63	64	B44	Cytoplasm	RNA binding
102	NENSLFKSL	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 CLH1_HUMAN	1050,54	53	B44	Cytoplasm	Cell growth and/or maintenance
103	AEELFARKF	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 CLH1_HUMAN	1109,59	34	B44	Cytoplasm	Cell growth and/or maintenance
104	KEIFLRELI	Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 ENPL_HUMAN	1159,69	38	B44	Endoplasmic reticulum	Protein metabolism
105	QEGDIILVL	Neutrophil cytosol factor 2 OS=Homo sapiens GN=NCF2 PE=1 SV=2 NCF2_HUMAN	998,56	44	B44	Cytoplasm	Metabolism ; Energy pathways
106	AEGAPSPNY	E3 ubiquitin-protein ligase CBL OS=Homo sapiens GN=CBL PE=1 SV=2 CBL_HUMAN	904,38	48	B44	Cytoplasm	Cell communication ; Signal transduction ; Protein metabolism
107	HEAEVLKQL	Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3 STMN1_HUMAN	1065,59	55	B44	Cytoplasm	Cell growth and/or maintenance ; Signal transduction
108	TEIEGTQKL	Protein-tyrosine kinase 2-beta OS=Homo sapiens GN=PTK2B PE=1 SV=2 FAK2_HUMAN	1017,51	39	B44	Cytoplasm	Signal transduction ; Cell communication
109	TEFRNFIVW	UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1	1210,62	29	B44	Nucleus	Transcription/Transcription regulation
110	NESEEVRQF	Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1 CPNS1_HUMAN	1136,49	27	B44	Cytoplasm	Protein folding
111	EERGFDKAY	Barrier-to-autointegration factor OS=Homo sapiens GN=BANF1 PE=1 SV=1 BAF_HUMAN	1113,51	30	B44	Nucleus	DNA binding
112	NENDIRVMF	CUGBP Elav-like family member 2 OS=Homo sapiens GN=CELF2 PE=1 SV=1 CELF2_HUMAN	1136,55	24	B44	Nucleus	RNA binding
113	AEDDFKKVL	DnaJ homolog subfamily C member 3 OS=Homo sapiens GN=DNAJC3 PE=1 SV=1 DNJC3_HUMAN	1063,54	14	B44	Cytoplasm	Protein metabolism
114	EEEVPKRKW	Genetic suppressor element 1 OS=Homo sapiens GN=GSE1 PE=1 SV=3 GSE1_HUMAN	1199,61	19	B44	unknown	unknown
115	EEPIFFDTW	Interleukin-1 beta OS=Homo sapiens GN=IL1B PE=1 SV=2	1182,52	22	B44	Extracellular	Immune response
116	EENRQKLSL	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 MYH9_HUMAN	1115,57	28	B44	Cytoplasm	Cell growth and/or maintenance

117	DENSVIKSF	Nucleolar protein 11 OS=Homo sapiens GN=NOL11 PE=1 SV=1 NOL11_HUMAN	1037,48	43	B44	Nucleolus	Transcription/Transcription regulation
118	REAEFTKSI	Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=3 SPCS2_HUMAN	1079,54	40	B44	Microsome	Protein metabolism
119	EEPTVIKKY	Sorting nexin-5 OS=Homo sapiens GN=SNX5 PE=1 SV=1 SNX5_HUMAN	1105,58	34	B44	Endosome	Transport
120	EEFLRQEHF	2'-5'-oligoadenylate synthase-like protein OASL_HUMAN	1233.5778	19	B44	Nucleus	Transcription/Transcription regulation
121	EELYTKKLW	26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2 PSD13_HUMAN	1208,65	48	B44	Cytoplasm	Protein metabolism
122	AETPDIKLF	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 RS5_HUMAN	1032,55	40	B44	Ribosome	Protein metabolism
123	EEFPGGLTI	5'-3' exoribonuclease 1 OS=Homo sapiens GN=XRN1 PE=1 SV=1	961,47	17	B44	Cytoplasm	Ribonuclease activity
124	EDNGIIKAF	60S ribosomal protein L4 RL4_HUMAN	1005.5131	60	B44	Ribosome	Protein metabolism
125	QELQEINRVY	Annexin A2.1 ANXA2.1_HUMAN	1290.6568	62	B44	Nucleus	Signal transduction ; Cell communication
126	QEFGVPHQY	Bifunctional protein NCOAT OS=Homo sapiens GN=MGEA5 PE=1 SV=2 NCOAT_HUMAN	1103,49	31	B44	Cytoplasm	Metabolism ; Energy pathways
127	EELPHIHAF	BolA-like protein 2 OS=Homo sapiens GN=BOLA2.1 PE=1 SV=1 BOLA2.1_HUMAN	1091,55	52	B44	exosome	unknown
128	EEIKKETGF	Calcineurin B homologous protein 1 OS=Homo sapiens GN=CHP1 PE=1 SV=3 CHP1_HUMAN	1079,53	32	B44	Membrane	Transport
129	AEIHLPHFI	Caspase recruitment domain-containing protein 8 OS=Homo sapiens GN=CARD8 PE=1 SV=1 CARD8_HUMAN	1075,57	29	B44	Cytoplasm	Apoptosis
130	KETEIVKKL	CCAAT/enhancer-binding protein zeta OS=Homo sapiens GN=CEBPZ PE=1 SV=3 CEBPZ_HUMAN	1086,65	42	B44	Nucleus	Transcription/Transcription regulation
131	DEALIGKKF	Chromodomain-helicase-DNA-binding protein 2 OS=Homo sapiens GN=CHD2 PE=1 SV=2 CHD2_HUMAN	1019,55	52	B44	Nucleus	DNA binding
132	QEFEHVNGRW	Chromodomain-helicase-DNA-binding protein 4 CHD4_HUMAN	1300.5949	50	B44	Nucleus	DNA binding

133	SEDKSIRVW	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2 COPA_HUMAN	1118,56	46	B44	Cytoplasm	Transport
134	SEWSHPIHW	Cytokine receptor common subunit gamma OS=Homo sapiens GN=IL2RG PE=1 SV=1 IL2RG_HUMAN	1177,58	41	B44	Plasma membrane	Immune response
135	AEGEINNVQW	DDB1- and CUL4-associated factor 7 DCAF7_HUMAN	1158.5305	47	B44	Cytoplasm	unknown
136	AEALSKMKL	DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5 MCM5_HUMAN	989,54	28	B44	Nucleus	DNA binding
137	EESDIVFHF	Eosinophil lysophospholipase OS=Homo sapiens GN=CLC PE=1 SV=3 LPPL_HUMAN	1121,49	51	B44	Secretory granule	Immune response
138	EEFRHVIAW	ETS translocation variant 3-like protein OS=Homo sapiens GN=ETV3L PE=2 SV=1 ETV3L_HUMAN	1185,6	34	B44	Nucleus	DNA binding protein
139	KENPLQFKF	Ezrin GN= EZR EZRI_HUMAN	1149,61	-	B44	Cytoplasm	Cell growth and/or maintenance
140	EEVLIPDQKY	F-box/LRR-repeat protein 3 FBXL3_HUMAN	1232.6288	51	B44	nucleus	Protein metabolism
141	NEAVLHLRF	F-box/WD repeat-containing protein 11 OS=Homo sapiens GN=FBXW11 PE=1 SV=1 FBW1B_HUMAN	1097,6	43	B44	Cytoplasm	Protein metabolism
142	NESLFGKKY	Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=1 SV=3 FHL2_HUMAN	1084,55	46	B44	Nucleus	Protein binding
143	EESDLSRQY	General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4 TF3C1_HUMAN	1125,48	46	B44	Nucleus	Transcription/Transcription regulation
144	VEELFERKY	General transcription factor II-I GN=GTF2IRD1 GTF2I_HUMAN	1211.6186	52	B44	Nucleus	Transcription/Transcription regulation
145	AENISRVLY	Glycogen phosphorylase, liver form PYGL_HUMAN	1063.5662	39	B44	Cytoplasm	Metabolism ; Energy pathways
146	AEGDLIEHF	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 ROA0_HUMAN	1029,48	54	B44	Nucleus	RNA binding
147	TENDIYNFF	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 HNRPF_HUMAN	1161,49	55	B44	Nucleus	Ribonucleoprotein
148	AENPGKYNL	heterogeneous nuclear ribonucleoprotein U isoform b GN=HNRNPU	1004,47	-	B44	Nucleus	RNA binding

149	EERVINEEY	Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3 RBBP4_HUMAN	1179,52	62	B44	Nucleus	Transcription/Transcription regulation
150	EEFGQAFSF	HLA class II histocompatibility antigen, DP alpha 1 chain OS=Homo sapiens GN=HLA-DPA1 PE=1 SV=1 DPA1_HUMAN	1060,44	18	B44	Plasma membrane	Immune response
151	AEVGRVYLF	Integrin alpha-IIb OS=Homo sapiens GN=ITGA2.1B PE=1 SV=3 ITA2.1B_HUMAN	1052,56	31	B44	Plasma membrane	Cell communication ; Signal transduction
152	IESGPGCTW	Integrin beta-2 GN= ITGB2 ITB2_HUMAN	948.4011	29	B44	Plasma membrane	Cell communication ; Signal transduction
153	NENHSGELW	Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2 ILK_HUMAN	1084,46	26	B44	Cytoplasm	Cell communication ; Signal transduction
154	ADARIFKAW	Interferon regulatory factor 7 OS=Homo sapiens GN=IRF7 PE=1 SV=2 IRF7_HUMAN	1076,58	29	B44	Cytoplasm	DNA binding
155	EEVQRKLGF	Interferon-induced protein 44 OS=Homo sapiens GN=IFI44 PE=2 SV=2 IFI44_HUMAN	1104,6	48	B44	Cytoplasm	unknown
156	EEKPNNPEF	Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 IFIT3_HUMAN	1102,48	24	B44	Cytoplasm	immune response
157	AEIRSLVTW	Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 IFIT3_HUMAN	1073,57	30	B44	Cytoplasm	immune response
158	EEVLIHGVSY	Kelch-like protein 22 GN=KLHL22 KLH22_HUMAN	1144.5764	39	B44	Cytoplasm	Cell growth and/or maintenance
159	QEVERILYF	Lysine-specific histone demethylase 1B OS=Homo sapiens GN=KDM1B PE=1 SV=3 KDM1B_HUMAN	1195,61	21	B44	Nucleus	Transcription/Transcription regulation
160	AETHIVLLF	Magnesium transporter protein 1 OS=Homo sapiens GN=MAGT1 PE=1 SV=1	1041,58	38	B44	Plasma membrane	Transport
161	EEGPPSTAL	Microtubule-associated protein 1A OS=Homo sapiens GN=MAP1A PE=1 SV=6 MAP1A_HUMAN	899,4	10	B44	Cytoplasm	Cell growth and/or maintenance
162	KEYEKALKY	Mitochondrial fission 1 protein OS=Homo sapiens GN=FIS1 PE=1 SV=2 FIS1_HUMAN	1170,61	46	B44	Mitochondrion	Apoptosis
163	KESPLLFKF	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 MOES_HUMAN	1107,63	46	B44	Cytoplasm	Cell growth and/or maintenance

164	KEFPSILRF	Myeloid differentiation primary response protein MyD88 OS=Homo sapiens GN=MYD88 PE=1 SV=1 MYD88_HUMAN	1135,63	29	B44	Nucleus	Cell communication ; Signal transduction
165	AEGPPRLAI	Myeloid leukemia factor 2 OS=Homo sapiens GN=MLF2 PE=1 SV=1 MLF2_HUMAN	922,51	25	B44	Nucleus	unknown
166	MEPEKLVHKF	Neurabin-2 GN=PPP1R9B NEB2_HUMAN	1256.6587	23	B44	Cytoplasm	Cell growth and/or maintenance
167	AEGDLVRLL	Neutrophil cytosol factor 4 OS=Homo sapiens GN=NCF4 PE=1 SV=2 NCF4_HUMAN	984,53	75	B44	Cytoplasm	Metabolism ; Energy pathways
168	TEVDNYHFY	Nuclear factor erythroid 2-related factor 2 GN= NFE2L2 NF2L2_HUMAN	1186.4931	40	B44	Nucleus	Transcription/Transcription regulation
169	EEQKNLHFF	Nuclear receptor-binding protein OS=Homo sapiens GN=NRBP1 PE=1 SV=1 NRBP_HUMAN	1190,58	68	B44	Nucleus	Cell communication ; Signal transduction
170	IEAELNKHW	Nucleoporin NUP188 homolog OS=Homo sapiens GN=NUP188 PE=1 SV=1 NU188_HUMAN	1138,56	23	B44	Nuclear membrane	unknown
171	EEAEWQTRW	Oxysterol-binding protein-related protein 2 OS=Homo sapiens GN=OSBPL2 PE=1 SV=1 OSBL2_HUMAN	1233,55	47	B44	endoplasmic reticulum	Transport
172	EELPTLLHF	Phosphoinositide 3-kinase adapter protein 1 OS=Homo sapiens GN=PIK3AP1 PE=1 SV=2	1097,58	34	B44	Cytoplasm	Cell communication ; Signal transduction
173	EELGFRPEY	Poly [ADP-ribose] polymerase 1 PARP1_HUMAN	1138.5295	43	B44	Nucleus	Transcription/Transcription regulation
174	EESGARINI	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 PCBP1_HUMAN	987,48	46	B44	Nucleus	RNA binding
175	SEEDLKVLF	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 PTBP1_HUMAN	1078,55	44	B44	Nucleus	Ribonucleoprotein
176	AEVDKVARL	Protein angel homolog 1 OS=Homo sapiens GN=ANGEL1 PE=1 SV=1 ANGE1_HUMAN	999,54	31	B44	unknown	unknown
177	MESDFEQKL	Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 DIAP1_HUMAN	1125,49	28	B44	Cytoplasm	Cell growth and/or maintenance
178	SEGNITKQL	Protein FAM65B OS=Homo sapiens GN=FAM65B PE=1 SV=4 FA65B_HUMAN	988,49	50	B44	membrane	Cell growth and/or maintenance
179	AENPFLTHL	Protein kinase C delta type OS=Homo sapiens GN=PRKCD PE=1 SV=2 KPCD_HUMAN	1040,53	41	B44	Cytosol	Cell communication ; Signal transduction
180	EEGPDVLRW	Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2 SC23A_HUMAN	1099,54	50	B44	Cytoplasm	Transport

181	QENLKPKQF	Protein-tyrosine kinase 2-beta OS=Homo sapiens GN=PTK2B PE=1 SV=2 FAK2_HUMAN	1130,59	49	B44	Cytoplasm	Signal transduction ; Cell communication
182	AEAFLEHLW	Putative RRN3-like protein FLJ77916 GN= RRN3P2 OS=Homo sapiens PE=5 SV=1	1114,55	31	B44	unknown	unknown
183	QEDLRTFSW	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1 G3BP1_HUMAN	1180,55	27	B44	Cytosol	Cell communication ; Signal transduction
184	NEFPEPIKL	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1 RAB7A_HUMAN	1085,57	25	B44	Endosome	Cell communication ; Signal transduction
185	EETPVVLQL	Renin receptor OS=Homo sapiens GN=ATP6AP2 PE=1 SV=2 RENR_HUMAN	1026,56	22	B44	Plasma membrane	Cell communication ; Signal transduction
186	EENKLVKKI	Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 SEPT7_HUMAN	1099,66	50	B44	Cytoskeleton	Cell communication ; Signal transduction
187	TEDDSLVVW	Serine/threonine-protein kinase Nek9 OS=Homo sapiens GN=NEK9 PE=1 SV=2 NEK9_HUMAN	1062,48	51	B44	Cytoplasm	Cell growth and/or maintenance
188	SECQHLIRW	Serine/threonine-protein kinase pim-1 OS=Homo sapiens GN=PIM1 PE=1 SV=3 PIM1_HUMAN	1170,57	41	B44	Plasma membrane	Cell communication ; Signal transduction ; Drug metabolism
189	AFDLTEQRY	Serine/threonine-protein kinase tousled-like 2 GN= TLK2 TLK2_HUMAN	1141.5404	36	B44	Nucleus	Cell communication ; Signal transduction
190	SEIHLQVKY	Sialoadhesin GN= SIGLEC1 SN_HUMAN	1115.5975	30	B44	Plasma membrane	Immune response
191	SESPIVVVL	Signal peptidase complex catalytic subunit SEC11A OS=Homo sapiens GN=SEC11A PE=1 SV=1 SC11A_HUMAN	941,54	35	B44	unknown	Protein metabolism
192	EELQQKVSY	Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2 STAT3_HUMAN	1122,53	34	B44	Nucleus	Transcription/Transcription regulation
193	SEAKAFHDY	Single-stranded DNA-binding protein 2 OS=Homo sapiens GN=SSBP2 PE=1 SV=2 SSBP2_HUMAN	1066,46	52	B44	Nucleus	Transcription/Transcription regulation
194	AETVQTVRY	Spartin OS=Homo sapiens GN=SPG20 PE=1 SV=1 SPG20_HUMAN	1065,51	58	B44	Cytoplasm	Transport
195	EEASLLHQF	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2 SPTB2_HUMAN	1072,52	32	B44	Cytoskeleton	Cell growth and/or maintenance
196	AEGKFWTHW	Splicing factor 3A subunit 2 OS=Homo sapiens GN=SF3A2.1 PE=1 SV=2 SF3A2.1_HUMAN	1160,54	46	B44	Nucleus	Protein metabolism

197	SENTRPKFL	Structural maintenance of chromosomes protein 6 OS=Homo sapiens GN=SMC6 PE=1 SV=2	1090,55	13	B44	Nucleus	DNA repair
198	SESLVHESW	SUN domain-containing protein 2 GN=SUN2 SUN2_HUMAN	1072.4825	29	B44	membrane	Cell organization and biogenesis
199	SEIEAKVRY	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 TLN1_HUMAN	1093,57	61	B44	Extracellular	Cell growth and/or maintenance
200	EEAPKFLAF	Trafficking protein particle complex subunit 6A OS=Homo sapiens GN=TRAPPC6A PE=1 SV=2 TPC6A_HUMAN	1050,53	24	B44	Golgi Apparatus/endoplasmic reticulum	Transport
201	AEELERQGY	Transcription elongation factor SPT6 OS=Homo sapiens GN=SUPT6H PE=1 SV=2 SPT6H_HUMAN	1093,49	51	B44	Nucleus	Transcription/Transcription regulation
202	AEALPKQSV	Transcription factor BTF3 OS=Homo sapiens GN=BTF3 PE=1 SV=1 BTF3_HUMAN	941,5	50	B44	Nucleus	Transcription/Transcription regulation
203	AEVKGVYQF	Transmembrane emp24 domain-containing protein 3 TMED3_HUMAN	1039.5338	30	B44	endoplasmic reticulum	Transport
204	EENTNILKF	Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1 TMOD3_HUMAN	1106,56	47	B44	Cytoplasm	Cell growth and/or maintenance
205	DEIERKFDKW	U4/U6 small nuclear ribonucleoprotein Prp31 GN=PRPF31 PRP31_HUMAN	1364.6724	53	B44	Nucleus	RNA binding
206	NELNIIHKF	U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=1 SV=2 PRP31_HUMAN	1126,63	25	B44	Nucleus	RNA binding
207	KESTLHLVL	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2 RS27A_HUMAN	1038,63	36	B44	Ribosome	Protein metabolism
208	EEIAFLKKL	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 VIME_HUMAN	1089,65	54	B44	Intermediate filament	Cell growth and/or maintenance
209	EELLFSHKL	WASH complex subunit FAM21B OS=Homo sapiens GN=FAM21B PE=1 SV=2 FA2.11B_HUMAN	1114,6	41	B44	unknown	Transport
210	SEDGKIHVW	WD repeat-containing protein 82 OS=Homo sapiens GN=WDR82 PE=1 SV=1 WDR82_HUMAN	1069,52	63	B44	Nucleus	cell cycle
211	AEAAASAYY	WW domain-binding protein 2 OS=Homo sapiens GN=WBP2 PE=1 SV=1 WBP2_HUMAN	915,39	52	B44	unknown	Cell communication ; Signal transduction

212	QYDEAVAQF	Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2 NASP_HUMAN	1069,46	39	B44	Nucleus	Cell communication ; Signal transduction
213	DEFKRLFAKY	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2 SFPQ_HUMAN	1315,69	20	B44	Nucleus	RNA binding
214	EELKETIKKL	Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1 DEK_HUMAN	1229,7	51	B44	Nucleus	DNA binding
215	SEGSFLLTTF	Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 NONO_HUMAN	1100,53	30	B44	Nucleus	RNA binding
216	EELNDLIQRF	Pericentriolar material 1 protein OS=Homo sapiens GN=PCM1 PE=1 SV=4 PCM1_HUMAN	1275,64	47	B44	Centrosome	Cell growth and/or maintenance
217	TEITDDLHFY	Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1 SND1_HUMAN	1252,56	32	B44	Nucleus	Transcription/Transcription regulation
218	MEQPIKVTEW	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 PLAK_HUMAN	1259,63	38	B44	Cytoplasm	Cell communication ; Signal transduction
219	TEHEPTKMFY	Protein polybromo-1 OS=Homo sapiens GN=PBRM1 PE=1 SV=1 PB1_HUMAN	1281,56	29	B44	Nucleus	Regulation of development
220	AEGTEEGARW	Protein OS-9 OS=Homo sapiens GN=OS9 PE=1 SV=1 OS9_HUMAN	1104,47	70	B44	Cytoplasm	Protein metabolism
221	ARLQKILHSF	5-methylcytosine rRNA methyltransferase GN= NSUN4 NSUN4_HUMAN	1211,72	-	B44	Mitochondrion RNA binding	
222	NEDNGIIKAF	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 RL4_HUMAN	1119,56	48	B44	Ribosome	protein metabolism
223	HEIYTVGKRF	60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 RL7_HUMAN	1248,64	35	B44	Ribosome	protein metabolism
224	AEAAGLHKVF	DNA topoisomerase 2-beta OS=Homo sapiens GN=TOP2B PE=1 SV=3 TOP2B_HUMAN	1041,55	36	B44	Nucleus	DNA topoisomerase activity
225	EESYFTTRTY	Emerin OS=Homo sapiens GN=EMD PE=1 SV=1 EMD_HUMAN	1295,55	35	B44	Nucleus	Cell growth and/or maintenance
226	AEGNNVVGLL	GLUCOKINASE OS=HOMO SAPIENS GN=GCK PE=1 SV=1	984,53	53	B44	Mitochondrion	Metabolism ; Energy pathways
227	AEADKTIKVY	Pleiotropic regulator 1 OS=Homo sapiens GN=PLRG1 PE=1 SV=1 PLRG1_HUMAN	1135,57	23	B44	Nucleus	Cell communication ; Signal transduction

228	NEVYEAVKNY	Protein polybromo-1 OS=Homo sapiens GN=PBRM1 PE=1 SV=1 PB1_HUMAN	1227,56	35	B44	Nucleus	Regulation of development
229	EEIDLRSVGW	Protein unc-93 homolog B1 OS=Homo sapiens GN=UNC93B1 PE=1 SV=2 UN93B_HUMAN	1202,59	43	B44	membrane	Transport
230	GEIWLAIHHF	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3	1221,65	42	B44	Nucleus	Protein metabolism
231	AEMGKGSFRY	1 EF1a-like protein	1144,56	-	B44	Cytoplasm	Transcription regulator activity
232	SEMRASLESW	2'-5'-oligoadenylate synthase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=3 OAS3_HUMAN	1194,54	39	B44	Cytoplasm	Immune response
233	AEKAVTKEEF	40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4 RSSA_HUMAN	1150,57	63	B44	Cytoplasm	Cell communication ; Signal transduction ; Cell adhesion
234	SEMNTDKQYF	60S ribosomal export protein NMD3 OS=Homo sapiens GN=NMD3 PE=1 SV=1 NMD3_HUMAN	1261,52	25	B44	Nucleolus	Transport
235	QEHIDLGIKY	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 RL11_HUMAN	1214,63	51	B44	Ribosome	Protein metabolism
236	AEGIHTGQFVY	60S ribosomal protein L8 gene= RPL8 RL8_HUMAN	1220.5826	36	B44	Nucleolus	Protein metabolism
237	GEAALGKRLW	Arachidonate 15-lipoxygenase OS=Homo sapiens GN=ALOX15 PE=1 SV=3 LOX15_HUMAN	1099,63	56	B44	Cytoplasm	Metabolism ; Energy pathways
238	EEFDARWVTY	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2 COX5A_HUMAN	1314,59	23	B44	Mitochondrion	Metabolism ; Energy pathways
239	AEIPADPKLY	Dedicator of cytokinesis protein 8 DOCK8_HUMAN	1115.5862	21	B44	Plasma membrane	Cell communication ; Signal transduction
240	SENKIVGIGY	Deoxycytidylate deaminase OS=Homo sapiens GN=DCTD PE=1 SV=2 DCTD_HUMAN	1078,54	48	B44	cytosol	Metabolism ; Energy pathways
241	MEQNTEGVKW	Deoxyhypusine synthase OS=Homo sapiens GN=DHPS PE=1 SV=1DHYS_HUMAN	1221,56	53	B44	unknown	Metabolism ; Energy pathways
242	SEGDITQKGY	Disco-interacting protein 2 homolog B OS=Homo sapiens GN=DIP2B PE=1 SV=3 DIP2B_HUMAN	1096,49	56	B44	unknown	unknown
243	AEDIAKIKKF	DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3 MCM3_HUMAN	1161,65	68	B44	Nucleus	DNA binding

244	GEDVETSKKW	Endothelial differentiation-related factor 1 OS=Homo sapiens GN=EDF1 PE=1 SV=1 EDF1_HUMAN	1177,56	73	B44	Nucleus	Transcription/Transcription regulation
245	QEIENAINEY	FERM domain-containing protein 4B OS=Homo sapiens GN=FRMD4B PE=1 SV=4 FRM4B_HUMAN	1221,54	33	B44	Plasma membrane	Signal transduction ; Cell communication
246	EEVRQGLKAY	Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2 GLRX3_HUMAN	1191,6	49	B44	Cytoplasm	unknown
247	INLKLKLHSF	Histone-binding protein RBBP4 GN= RBBP4 RBBP4_HUMAN	1211,72	-	B44	Nucleus	Transcription regulation
248	SEALALTQTW	HLA class I histocompatibility antigen, alpha chain E OS=Homo sapiens GN=HLA-E PE=1 SV=3 HLAE_HUMAN	1118,57	58	B44	Plasma membrane	Immune response
249	SEAGSHTLQW	HLA class I histocompatibility antigen, Cw-14 alpha chain OS=Homo sapiens GN=HLA-C PE=2 SV=2 1C14_HUMAN	1114,5	11	B44	Plasma membrane	Immune response
250	QEIECQNQEY	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 K1C9_HUMAN	1282,5	49	B44	Cytoplasm	Cell growth and/or maintenance
251	YEVEIDGKTY	Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1 AMPM2_HUMAN	1215,57	60	B44	unknown	Protein metabolism
252	AEFKEAFQLF	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	1228,62	35	B44	Cytoplasm	Cell growth and/or maintenance
253	AEIRHVLVTL	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2 MYL6_HUMAN	1149,66	63	B44	Cytoplasm	Cell growth and/or maintenance
254	QEYPDLIHIY	Nuclear autoantigen Sp-100 OS=Homo sapiens GN=SP100 PE=1 SV=3 SP100_HUMAN	1289,62	24	B44	Nucleus	Transcription/Transcription regulation
255	EEVHDLERKY	Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1 NP1L1_HUMAN	1316,64	58	B44	Nucleus	DNA binding
256	GEWASGGVRSF	Peroxiredoxin-5, mitochondrial GN=PRDX5 PRDX5_HUMAN	1151.5360	63	B44	Mitochondrion	Metabolism ; Energy pathways
257	AEQTALMAKY	Peroxisomal proliferator-activated receptor A-interacting complex 285 kDa protein OS=Homo sapiens GN=PRIC285 PE=1 SV=6 PR285_HUMAN	1124,53	39	B44	Nucleus	unknown
258	AEDPLGAIHL	Pleckstrin OS=Homo sapiens GN=PLEK PE=1 SV=3 PLEK_HUMAN	1034,53	53	B44	Plasma membrane	Cell communication ; Signal transduction

259	SEEAEIIRKY	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 PARP1_HUMAN	1236,62	82	B44	Nucleus	Transcription/Transcription regulation
260	AEHPTIKIFW	Probable E3 ubiquitin-protein ligase HERC4 OS=Homo sapiens GN=HERC4 PE=1 SV=1 HERC4_HUMAN	1240,67	16	B44	Cytoplasm	Protein metabolism
261	DEHEGPALYY	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1 PSB2_HUMAN	1192,49	38	B44	Cytoplasm	Protein metabolism
262	GESSFTYRAY	Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=2 SCAFB_HUMAN	1179,51	57	B44	Nucleus	mRNA processing
263	TEFEDIKSGY	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 SET_HUMAN	1187,52	37	B44	Nucleus	MHC class I receptor activity
264	EEILKVEQKY	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 SET_HUMAN	1277,68	75	B44	Nucleus	MHC class I receptor activity
265	EEIHATGFNY	Puromycin-sensitive aminopeptidase-like protein OS=Homo sapiens GN=NPEPPSL1 PE=2 SV=3 PSAL_HUMAN	1179,5	28	B44	exosome	protein metabolism
266	EEPQHVLLRY	Regulator of nonsense transcripts 1 GN=UPF1 RENT1_HUMAN	1282.6670	37	B44	Cytoplasm	Regulation of translation ; RNA metabolism
267	DEAPVLDVRY	REST corepressor 1 OS=Homo sapiens GN=RCOR1 PE=1 SV=1 RCOR1_HUMAN	1175,57	58	B44	Nucleus	Transcription/Transcription regulation
268	AEFTKSIAKF	Signal peptidase complex subunit 2 GN= SPCS2 SPCS2_HUMAN	1140.6179	45	B44	Microsome	Protein metabolism
269	GEIDQQYSRF	Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2 STAT3_HUMAN	1241,55	45	B44	Nucleus	Transcription/Transcription regulation
270	AELDRQIKSF	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3 SPTN1_HUMAN	1205,62	50	B44	Cytoplasm	Cell growth and/or maintenance
271	QETSFTKEAY	TPT1-like protein OS=Homo sapiens PE=1 SV=2 TPT1L_HUMAN	1202,55	48	B44	exosome	unknown
272	DEFSHQVQEW	Transcription elongation factor SPT6 OS=Homo sapiens GN=SUPT6H PE=1 SV=2 SPT6H_HUMAN	1303.5469	34	B44	Nucleus	Transcription/Transcription regulation
273	SESTNQRVLW	Transmembrane emp24 domain-containing protein 9 TMED9_HUMAN	1218.5993	21	B44	Endoplasmic reticulum	Transport

274	SEPDFVAKFY	Uncharacterized protein C14orf119 OS=Homo sapiens GN=C14orf119 PE=2 SV=1 CN119_HUMAN	1201,56	37	B44	mitochondrion	unknown
275	NEIEDTFRQF	V-type proton ATPase subunit F OS=Homo sapiens GN=ATP6V1F PE=1 SV=2 VATF_HUMAN	1297,61	55	B44	Plasma membrane	Metabolism ; Energy pathways
276	EEDPNTHILY	Zinc finger and BTB domain-containing protein 17 OS=Homo sapiens GN=ZBTB17 PE=1 SV=3 ZBT17_HUMAN	1229,54	21	B44	Nucleus	Transcription/Transcription regulation
277	VELDDLGKDEL	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 PDIA6_HUMAN	1244,6	47	B44	Endoplasmic reticulum	Protein metabolism
278	SEFLATKAKQF	Poly [ADP-ribose] polymerase 9 PARP9_HUMAN	1268.6765	42	B44	Nucleus	DNA repair
279	AEAQLRFIQAW	Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1 URP2_HUMAN	1331,69	47	B44	Plasma membrane	unknown
280	SETSVPDHVVW	Interferon-induced transmembrane protein 1 OS=Homo sapiens GN=IFITM1 PE=1 SV=3 IFM1_HUMAN	1254,6	37	B44	Plasma membrane	Cell communication ; Signal transduction
281	AEDENGKIVGY	N-alpha-acetyltransferase 10 OS=Homo sapiens GN=NAA10 PE=1 SV=1 NAA10_HUMAN	1192,52	35	B44	Cytoplasm	Metabolism ; Energy pathways
282	EEFSRAAEKLY	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 SRP09_HUMAN	1341,63	28	B44	Cytoplasm	Protein metabolism
283	EEAQFETKKLY	15 kDa selenoprotein OS=Homo sapiens GN=SEP15 PE=1 SV=3 SEP15_HUMAN	1384,68	64	B44	Endoplasmic reticulum	Protein folding
284	DEIDAIGGRRF	26S protease regulatory subunit 10B Gene= PSMC6 PRS10_HUMAN	1247.6258	38	B44	Cytoplasm	Protein metabolism
285	EEIAIIPSKKL	40S ribosomal protein S17-like RS17L_HUMAN	1239.7438	50	B44	Ribosome	Protein metabolism
286	NEDEDSPNKLY	60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1 RL31_HUMAN	1322,55	42	B44	Ribosome	Protein metabolism
287	EEDEDAYKKQF	60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3 RL5_HUMAN	1400,6	62	B44	Ribosome	Protein metabolism
288	AEDEGVSQRKF	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 CLIC1_HUMAN	1264,59	61	B44	Nucleus	Transport
289	EEKSIDLIQKW	Choline-phosphate cytidylyltransferase A OS=Homo sapiens GN=PCYT1A PE=1 SV=2 PCY1A_HUMAN	1387,73	33	B44	Nucleus	Metabolism ; Energy pathways

290	DETDSGAGLKW	DNA fragmentation factor subunit alpha OS=Homo sapiens GN=DFFA PE=1 SV=1 DFFA_HUMAN	1177,51	60	B44	Cytoplasm	Protein metabolism
291	GEIDLAKLKKF	DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5 MCM5_HUMAN	1260,74	60	B44	Nucleus	DNA binding
292	SESLFVSNHAY	Fructose-bisphosphate aldolase A ALDOA_HUMAN	1252.5724	55	B44	Cytoplasm	Metabolism ; Energy pathways
293	TENTEENRRFY	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 ALDOA_HUMAN	1457,65	26	B44	Cytoplasm	Metabolism ; Energy pathways
294	TEQSQIKGYVW	Gamma-secretase subunit PEN-2 OS=Homo sapiens GN=PSENEN PE=1 SV=1 PEN2_HUMAN	1337,67	29	B44	Endoplasmic reticulum	Protein metabolism
295	RENTQTTIKLF	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 HNRPK_HUMAN	1349,74	45	B44	Nucleus	Ribonucleoprotein
296	NEISERVVQHF	Inositol 1,4,5-trisphosphate receptor type 2 OS=Homo sapiens GN=ITPR2 PE=1 SV=2 ITPR2_HUMAN	1356,68	53	B44	Plasma membrane	Cell communication ; Signal transduction
297	SEADARIFKAW	Interferon regulatory factor 7 OS=Homo sapiens GN=IRF7 PE=1 SV=2 IRF7_HUMAN	1292,67	68	B44	Cytoplasm	DNA binding
298	DEMTGYVATRW	Mitogen-activated protein kinase 14 OS=Homo sapiens GN=MAPK14 PE=1 SV=3 MK14_HUMAN	1327,61	56	B44	Cytoplasm	Cell communication ; Signal transduction
299	QEAASLLGKKY	Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2 NASP_HUMAN	1206,65	80	B44	Nucleus	Cell communication ; Signal transduction
300	TEHYDIPKVSW	Protein FAM32A OS=Homo sapiens GN=FAM32A PE=1 SV=2 FA32A_HUMAN	1373,67	36	B44	Nucleus	Apoptosis; cell cycle
301	NELGVGGTSQW	Protein transport protein Sec23B SC23B_HUMAN	1146.5306	58	B44	Endoplasmic reticulum	Transport
302	QEFEEKSGRTF	RNA polymerase II subunit A C-terminal domain phosphatase SSU72 OS=Homo sapiens GN=SSU72 PE=1 SV=1 SSU72_HUMAN	1356,62	51	B44	Nucleus	mRNA processing
303	EEAQVRKENQW	S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2 SKP1_HUMAN	1415,67	57	B44	Nucleus	Protein metabolism
304	SEQRDYIDTTW	Surfeit locus protein 4 GN= SURF4 SURF4_HUMAN	1412.6208	40	B44	Endoplasmic reticulum	Transport

305	AEDLNTRVAYW	Transmembrane emp24 domain-containing protein 7 OS=Homo sapiens GN=TMED7 PE=1 SV=2 TMED7_HUMAN	1336,65	50	B44	endoplasmic reticulum	Transport
306	QESEDTAKAGF	Tyrosine-protein phosphatase non-receptor type 6 OS=Homo sapiens GN=PTPN6 PE=1 SV=1 PTN6_HUMAN	1181,51	50	B44	Cytoplasm	Cell communication ; Signal transduction
307	AEIGEGAYGKVF	Cyclin-dependent kinase 6 OS=Homo sapiens GN=CDK6 PE=1 SV=1 CDK6_HUMAN	1239,61	70	B44	Nucleus	Cell communication ; Signal transduction
308	AETDLSQGVARW	Extended synaptotagmin-1 ESYT1_HUMAN	1331.6470	68	B44	Plasma membrane	Cell communication ; Signal transduction
309	GEIDGNKVTLDW	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 NUCL_HUMAN	1345,65	37	B44	Nucleolus	RNA binding
310	QELDSTDGAKVF	Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=1 SV=1 SRP54_HUMAN	1308,6	55	B44	Cytoplasm	Protein metabolism
311	AEMGKGSFRYASV	Elongation factor 1-alpha 2 GN=EEF1A2.1 EF1A2.1_HUMAN	1401,68	-	B44	Cytoplasm	Protein metabolism
312	PELAVQKVVVHPLVL	26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2 PSD7_HUMAN	1639,99	73	B44	Nucleus	Protein metabolism
313	SFDTGFTSF	DnaJ homolog subfamily B member 6 OS=Homo sapiens GN=DNAJB6 PE=1 SV=2 DNJB6_HUMAN	1007,43	42	B56	Cytoplasm	Protein metabolism
314	RALKLKLHSF	Unnamed protein product	1211,72	-	B56	unkown	unkown
315	DIYNFF	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 HNRPF_HUMAN	817,36	15	#	Nucleus	Ribonucleoprotein
316	IQDLWQW	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	987,49	-	#	Nucleolus	Protein metabolism
317	EEEIAAL	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 ACTG_HUMAN	773,35	33	#	Cytoplasm	Cell growth and/or maintenance
318	AEIIRKY	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 PARP1_HUMAN	891,5	36	#	Nucleus	Transcription/Transcription regulation

319	YFDEPVEL	ADP-ribosylation factor GTPase-activating protein 3 OS=Homo sapiens GN=ARFGAP3 PE=1 SV=1 ARFG3_HUMAN	1010,47	38	#	cytoplasm	protein metabolism
320	IAKIPNFW	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 SET_HUMAN	987,55	42	#	Nucleus	MHC class I receptor activity
321	FFDDPMLL	116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1	996,47	23	#	Nucleus	Protein metabolism
322	NTDEMVEL	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 HNRPK_HUMAN	949,4	32	#	Nucleus	Ribonucleoprotein
323	LKLKLHSF	Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3 RBBP4_HUMAN	984,6	53	#	Nucleus	Transcription/Transcription regulation
324	SWEDAAILL	Cytokine receptor common subunit beta OS=Homo sapiens GN=CSF2RB PE=1 SV=2 IL3RB_HUMAN	1016,51	31	#	Plasma membrane	Cell communication ; Signal transduction
325	NLKLKLHSF	Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3 RBBP4_HUMAN	1098,68	46	#	Nucleus	Transcription/Transcription regulation
326	KFDDIRIYF	NFX1-type zinc finger-containing protein 1 OS=Homo sapiens GN=ZNFX1 PE=1 SV=2 ZNFX1_HUMAN	1215,62	49	#	Nucleus	Transcription/Transcription regulation
327	SEIDVSSEGVKGAKSF	EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1 EFHD2_HUMAN	1638,8	82	#	Nucleus and Cytoplasm	unknown

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No.	Peptide sequence	Protein name	Observed Mass[M+H]+	Mascot Score	HLA	Subcellular localisation	Biological function
1	KIEDGKAV	Cyclin-G-associated kinase OS=Homo sapiens GN=GAK PE=1 SV=2 GAK_HUMAN	858.4680	33	A2.1	Cytoplasm	Cell communication ; Signal transduction
2	EVWAAIPM	FYVE, RhoGEF and PH domain-containing protein 3 OS=Homo sapiens GN=FGD3 PE=1 SV=1 FGD3_HUMAN	915,39	13	A2.1	Cytoplasm	Cell communication ; Signal transduction
3	NIMSVVGV*	Guanylate cyclase soluble subunit alpha-3 OS=Homo sapiens GN=GUCY1A3 PE=1 SV=2 GCYA3_HUMAN	833.4597	42	A2.1	Cytoplasm	Cell communication ; Signal transduction
4	KVASLIGV	Dipeptidase 1 OS=Homo sapiens GN=DPEP1 PE=1 SV=3 DPEP1_HUMAN	785,47	47	A2.1	Endoplasmic reticulum	Protein metabolism
5	SISWDDRV	Hemicentin-1 OS=Homo sapiens GN=HMCN1 PE=1 SV=2 HMCN1_HUMAN	976.4602	28	A2.1	Extracellular	Cell communication ; Signal transduction
6	ALPFVLLM*	Interferon alpha-5 OS=Homo sapiens GN=IFNA5 PE=1 SV=1 IFNA5_HUMAN	918.5274	35	A2.1	Extracellular	Immune response
7	KLQLLAVV	Heparan sulfate 2-O-sulfotransferase 1 OS=Homo sapiens GN=HS2ST1 PE=1 SV=1 HS2ST_HUMAN	882.5416	29	A2.1	Golgi apparatus	Metabolism ; Energy pathways
8	PWNLVALS	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3 HEXB_HUMAN	898.4923	31	A2.1	Lysosome	Metabolism ; Energy pathways
9	LLTDLKEQ	DNA-DIRECTED RNA POLYMERASE III SUBUNIT RPC9 OS=HOMO SAPIENS GN=CRCP PE=1 SV=1RPC9_HUMAN	958,58	48	A2.1	Membrane	Cell communication ; Signal transduction
10	ITGVVITL	CYTOCHROME B-245 HEAVY CHAIN OS=HOMO SAPIENS GN=CYBB PE=1 SV=2CY24B_HUMAN	814,51	34	A2.1	Plasma membrane	Metabolism ; Energy pathways
11	VLDDKLVFV	ANOCTAMIN-6 OS=HOMO SAPIENS GN=ANO6 PE=1 SV=2ANO6_HUMAN	1046,61	16	A2.1	Membrane	unknown
12	QGIAILAVV	ANOCTAMIN-6 OS=HOMO SAPIENS GN=ANO6 PE=1 SV=2ANO6_HUMAN	882,54	27	A2.1	Membrane	unknown
13	TGPVATEVV	NACHT, LRR and PYD domains-containing protein 1 OS=Homo sapiens GN=NLRP1 PE=1 SV=1 NALP1_HUMAN	871.4851	34	A2.1	Cytoplasm	Apoptosis
14	VFDEAIRAV	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1 RAC1_HUMAN	1018,55	45	A2.1	Cytoplasm	Cell communication ; Signal transduction
15	ALSNLEVKL	Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1 URP2_HUMAN	985.5814	28	A2.1	Plasma membrane	cell adhesion

16	KLFNKFIGK	Neudesin OS=Homo sapiens GN=NENF PE=1 SV=1 NENF_HUMAN	809.4638	24	A2.1	Extracellular	unknown
17	ALPPVLTTV	La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2 LARP1_HUMAN	909.5489	33	A2.1	Nucleus	Transport
18	ALPPVLTTV	La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2 LARP1_HUMAN	909.5443	23	A2.1	Nucleus	Transport
19	SLAEGLRTV	2'-5'-oligoadenylate synthase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=3 OAS3_HUMAN	944,54	59	A2.1	Cytoplasm	Immune response
20	FASHVSPEV	ADP-ribosylation factor GTPase-activating protein 3 OS=Homo sapiens GN=ARFGAP3 PE=1 SV=1 ARFG3_HUMAN	971,52	58	A2.1	Cytoplasm	Protein metabolism
21	MVIQIQPPN	Arachidonate 12-lipoxygenase, 12S-type OS=Homo sapiens GN=ALOX12 PE=1 SV=4 LOX12_HUMAN	1038.6182	25	A2.1	Cytoplasm	Metabolism ; Energy pathways
22	VISQGKIVL	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 DPYL2_HUMAN	955.5732	26	A2.1	Cytoplasm	Cell communication ; Signal transduction
23	ALASHLIEA	EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2 EHD2_HUMAN	923,51	37	A2.1	Cytoplasm	Cell communication ; Signal transduction
24	ILTDITKGV	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 EF2_HUMAN	958,58	48	A2.1	Cytoplasm	Protein metabolism
25	ILTDITKGV	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 EF2_HUMAN	958,58	34	A2.1	Cytoplasm	Protein metabolism
26	VLMTEDIKL*	Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 IF4G1_HUMAN	1076,6	53	A2.1	Cytoplasm	Protein metabolism
27	ALSDHHIYL	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 ALDOA_HUMAN	1067,55	32	A2.1	Cytoplasm	Metabolism ; Energy pathways
28	ALDSQVPKV	FYVE, RhoGEF and PH domain-containing protein 3 OS=Homo sapiens GN=FGD3 PE=1 SV=1 FGD3_HUMAN	955,53	37	A2.1	Cytoplasm	Cell communication ; Signal transduction
29	NLAENISRV	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 PYGL_HUMAN	1014,55	49	A2.1	Cytoplasm	Metabolism ; Energy pathways
30	VMDSKIVQV	Importin subunit alpha-1 OS=Homo sapiens GN=KPNA1 PE=1 SV=3 IMA1_HUMAN	1017.5588	38	A2.1	Cytoplasm	Transport
31	LAGTALAAL	L-fucose kinase OS=Homo sapiens GN=FUK PE=2 SV=2 FUK_HUMAN	799.4774	28	A2.1	Cytoplasm	Metabolism ; Energy pathways
32	GLIDRQVTV	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4 MACF1_HUMAN	999.5603	26	A2.1	Cytoplasm	Cell communication ; Signal transduction
33	GLATDVQTV	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2 PSB3_HUMAN	902.4675	44	A2.1	Cytoplasm	Protein metabolism

34	LLMDTFFQI*	Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2 SC23A_HUMAN	1142,6	15	A2.1	Cytoplasm	Transport
35	QQVQAPVEL	PROTEIN-ARGININE DEIMINASE TYPE-1 OS=HOMO SAPIENS GN=PADI1 PE=1 SV=2	1010,46	24	A2.1	Cytoplasm	Metabolism ; Energy pathways
36	TLSDLRVYL	Sulfiredoxin-1 OS=Homo sapiens GN=SRXN1 PE=1 SV=2 SRXN1_HUMAN	1078.6028	27	A2.1	Cytoplasm	ATP binding
37	TLDEATPTL	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1 OS=Homo sapiens GN=TAB1 PE=1 SV=1 TAB1_HUMAN	959.4626	32	A2.1	Cytoplasm	Regulation of protein kinase activity
38	YIMGYISKV*	Unconventional myosin-If OS=Homo sapiens GN=MYO1F PE=1 SV=3 MYO1F_HUMAN	1088.5730	33	A2.1	Cytoplasm	Cell growth and/or maintenance
39	LLIENVASL	Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 PE=1 SV=4 GPX1_HUMAN,	970.5586	25	A2.1	Cytosol	Protein metabolism
40	ALADGVQKV	Apolipoprotein L1 OS=Homo sapiens GN=APOL1 PE=1 SV=5 APOL1_HUMAN	899,51	56	A2.1	Extracellular	Transport
41	YGNTLVEFR	Olfactomedin-like protein 2B OS=Homo sapiens GN=OLFML2B PE=2 SV=2 OLM2B_HUMAN	1097.5593	26	A2.1	Extracellular	unknown
42	GLDGPPPTV	Tumor necrosis factor alpha-induced protein 2 OS=Homo sapiens GN=TNFAIP2 PE=1 SV=2 TNAP2_HUMAN	851.4340	33	A2.1	Extracellular	unknown
43	AIVDKVPSV	Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 COPG1_HUMAN	926.5428	33	A2.1	Golgi apparatus	Transport
44	KLMDHIYAV*	Conserved oligomeric Golgi complex subunit 5 OS=Homo sapiens GN=COG5 PE=1 SV=3 COG5_HUMAN	1104.5867	28	A2.1	Golgi apparatus	Transport
45	ILFGHENRV	Guanine nucleotide-binding protein subunit beta-5 OS=Homo sapiens GN=GNB5 PE=1 SV=2 GBB5_HUMAN	1083.6003	43	A2.1	Membrane	Signal transduction ; Cell communication
46	LISDPVLLV	Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6 GCN1L_HUMAN	967.5144	41	A2.1	Nucleolus	Transciption regulation
47	VFDPVPVGV	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 DHX9_HUMAN,	927.5048	33	A2.1	Nucleus	Transcription factor activity
48	LLGPPPVGV	Cip1-interacting zinc finger protein OS=Homo sapiens GN=CIZ1 PE=1 SV=2	847.5178	32	A2.1	Nucleus	DNA binding
49	ELCPLAEEL	E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 TRI25_HUMAN	1015.5195	31	A2.1	Nucleus	Transcription factor activity
50	SLYEMVSRV*	FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1 SSRP1_HUMAN	1098.5498	29	A2.1	Nucleus	Transcription factor activity

51	SMYDKVLML	General transcription factor 3C polypeptide 5 OS=Homo sapiens GN=GTF3C5 PE=1 SV=2 TF3C5_HUMAN	1130.5471	34	A2.1	Nucleus	Transcription factor activity
52	SLLDKIIGA	Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1 PTRF_HUMAN	928,56	55	A2.1	Nucleus	Transcription regulator activity
53	SLLDKIIGA	Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1 PTRF_HUMAN	928,56	46	A2.1	Nucleus	Transcription regulator activity
54	SIYPSPTGV	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 PRP8_HUMAN	919,45	41	A2.1	Nucleus	RNA binding
55	SMSADVPLV*	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 PCNA_HUMAN	933.4422	31	A2.1	Nucleus	Cell growth and/or maintenance
56	QLAQFVHEV	Putative ATP-dependent RNA helicase DDX11-like protein 8 OS=Homo sapiens GN=DDX11L8 PE=1 SV=1 D11L8_HUMAN	1069,57	30	A2.1	Nucleus	unknown
57	TLADVLYHV	Set1/Ash2 histone methyltransferase complex subunit ASH2 OS=Homo sapiens GN=ASH2L PE=1 SV=1 ASH2L_HUMAN	1029,56	48	A2.1	Nucleus	DNA binding
58	IMLEALERV*	Small nuclear ribonucleoprotein G-like protein OS=Homo sapiens GN= SNRPGP15 PE=3 SV=2 RUXGL_HUMAN	1088,6	38	A2.1	Nucleus	unknown
59	FQDPVPLTV	Transcription intermediary factor 1-alpha OS=Homo sapiens GN=TRIM24 PE=1 SV=3 TIF1A_HUMAN	1014.5301	33	A2.1	Nucleus	Transcription regulator activity
60	TLADLVHHV	Transformation/transcription domain-associated protein OS=Homo sapiens GN=TRRAP PE=1 SV=3 TRRAP_HUMAN	1003,56	33	A2.1	Nucleus	Transcription regulator activity
61	LLFDRPMHV*	Zinc finger and BTB domain-containing protein 17 OS=Homo sapiens GN=ZBTB17 PE=1 SV=3 ZBT17_HUMAN	1229.5528	20	A2.1	Nucleus	Transcription regulator activity
62	VMAPRTLIL*	HLA class I histocompatibility antigen, Cw-3 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=2 1C03_HUMAN	1028.6245	21	A2.1	Plasma membrane	Immune response
63	LLPPQPALA	Angiotensin-converting enzyme OS=Homo sapiens GN=ACE PE=1 SV=1 ACE_HUMAN	918.5515	32	A2.1	Plasma membrane	Protein metabolism
64	SLDGAPIGV	Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2 PE=1 SV=1 E41L2_HUMAN	827.4385	30	A2.1	Plasma membrane	Cell communication ; Signal transduction
65	TLLAGITGV	CYTOCHROME B-245 HEAVY CHAIN OS=HOMO SAPIENS GN=CYBB PE=1 SV=2CY24B_HUMAN	843,5	16	A2.1	Plasma membrane	Metabolism ; Energy pathways
66	KLLTEVHAA	Disintegrin and metalloproteinase domain-containing protein 8 OS=Homo sapiens GN=ADAM8 PE=1 SV=2 ADAM8_HUMAN	980,59	39	A2.1	Plasma membrane	Protein metabolism
67	VMAPRTLVL*	HLA class I histocompatibility antigen, A-2 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1 1A02_HUMAN	1014.6104	26	A2.1	Plasma membrane	Immune response

68	VLSSRLAFA	HLA class II histocompatibility antigen, DR beta 3 chain OS=Homo sapiens GN=HLA-DRB3 PE=1 SV=1 DRB3_HUMAN	962.5633	42	A2.1	Plasma membrane	Immune response
69	QMKLDDICL	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 ITB2_HUMAN	1077.5276	37	A2.1	Plasma membrane	Cell communication ; Signal transduction
70	SMLDDLRNV*	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 ITB2_HUMAN	1077,53	17	A2.1	Plasma membrane	Cell communication ; Signal transduction
71	RLSQELPEV	Neuroblastoma breakpoint family member 4 OS=Homo sapiens GN=NBPF4 PE=2 SV=2 NBPF4_HUMAN	1069.5296	33	A2.1	Plasma membrane	Cell communication ; Signal transduction
72	ILHDDEVTV	60S ACIDIC RIBOSOMAL PROTEIN P1 OS=HOMO SAPIENS GN=RPLP1 PE=1 SV=1RLA1_HUMAN	1039,52	40	A2.1	Ribosome	Protein metabolism
73	TLYEAVREV	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 RL10A_HUMAN	1078.5582	35	A2.1	Ribosome	Protein metabolism
74	ILMEHIHKL*	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1RL19_HUMAN	1148.6568	40	A2.1	Ribosome	Structural constituent of ribosome
75	GLGPPGRSV	Protein SPT2 homolog OS=Homo sapiens GN=SPTY2D1 PE=1 SV=3 SPT2_HUMAN	838.4669	43	A2.1	unknown	unknown
76	LLPPPTLGP	Ras and Rab interactor-like protein OS=Homo sapiens GN=RINL PE=2 SV=1 RINL_HUMAN	903.4779	33	A2.1	unknown	unknown
77	LMRGEPFAS*	RNA-binding protein 41 OS=Homo sapiens GN=RBM41 PE=1 SV=2 RBM41_HUMAN	1022.5023	25	A2.1	unknown	RNA binding
78	GVSAWLNHL	TBC1 domain family member 16 OS=Homo sapiens GN=TBC1D16 PE=1 SV=1 TBC16_HUMAN	995.5169	28	A2.1	unknown	unknown
79	VLLSGTIRFN	ATP-binding cassette sub-family C member 11 OS=Homo sapiens GN=ABCC11 PE=1 SV=1 ABCCB_HUMAN	1118.6133	28	A2.1	Membrane	Transport
80	SLNTWLILCS	Piwi-like protein 4 OS=Homo sapiens GN=PIWIL4 PE=2 SV=2 PIWL4_HUMAN	1148.5972	29	A2.1	Cytoplasm	Protein metabolism
81	ISLEVDTGRT	PROTEIN-ARGININE DEIMINASE TYPE-1 OS=HOMO SAPIENS GN=PADI1 PE=1 SV=3	1089,63	27	A2.1	Cytoplasm	Metabolism ; Energy pathways
82	TTGVSVIMNT*	Serine/threonine-protein kinase DCLK2 OS=Homo sapiens GN=DCLK2 PE=2 SV=4 DCLK2_HUMAN	1037.5023	36	A2.1	Cytoplasm	Metabolism ; Energy pathways
83	ATSSPPNDIS	Serine/threonine-protein kinase WNK1 OS=Homo sapiens GN=WNK1 PE=1 SV=2 WNK1_HUMAN	987.4833	27	A2.1	Cytoplasm	Cell communication ; Signal transduction
84	LKFNKIVHSS	Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2 PGAM5_HUMAN	1171.6092	29	A2.1	Cytosol	Metabolism ; Energy pathways

85	QNMPETLPNN	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 13B OS=HOMO SAPIENS GN=TNFSF13B PE=1 SV=1TN13B_HUMAN	1156,55	24	A2.1	Extracellular	Cell communication ; Signal transduction
86	QSATVFMSEV*	Calmodulin-binding transcription activator 1 OS=Homo sapiens GN=CAMTA1 PE=1 SV=4 CMTA1_HUMAN	1113.5642	27	A2.1	Nucleus	Cell growth and/or maintenance
87	KRVLLYVRKE	Grainyhead-like protein 2 homolog OS=Homo sapiens GN=GRHL2 PE=1 SV=1 GRHL2_HUMAN	1302,69	20	A2.1	Nucleus	Transcription factor activity
88	LLDKVADNLA	Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3 ILF3_HUMAN,	1070.6873	28	A2.1	Nucleus	Transcription regulator activity
89	GLAAGGIVAV	MKL/myocardin-like protein 2 OS=Homo sapiens GN=MKL2 PE=1 SV=3	826.4872	32	A2.1	Nucleus	Transcription factor activity
90	AMFDHIPVGV*	tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=C22orf28 PE=1 SV=1 RTCB_HUMAN	1100,54	38	A2.1	Nucleus	unknown
91	SLLGGDVVSV	TSC22 domain family protein 3 OS=Homo sapiens GN=TSC22D3 PE=1 SV=2 T22D3_HUMAN	944,52	46	A2.1	Nucleus	Transcription regulator activity
92	NTAEGTAFRL	Protocadherin beta-9 OS=Homo sapiens GN=PCDHB9 PE=2 SV=2 PCDB9_HUMAN	1078.5430	26	A2.1	Plasma membrane	Cell communication ; Signal transduction
93	SLMDHTIPEV*	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1 DCB1_HUMAN	1156.5479	39	A2.1	Plasma membrane	Cell communication ; Signal transduction
94	KLLASDAEALS	Lipase maturation factor 1 OS=Homo sapiens GN=LMF1 PE=1 SV=1 LMF1_HUMAN	1116.7046	25	A2.1	Membrane	protein metabolism
95	DIAIDDLSFMD*	MAM and LDL-receptor class A domain-containing protein C10orf112 OS=Homo sapiens GN=C10orf112 PE=2 SV=3 CJ112_HUMAN	1269.6124	35	A2.1	Membrane	Metabolism ; Energy pathways
96	IIEDVMVK	Endonuclease domain-containing 1 protein OS=Homo sapiens GN=ENDOD1 PE=1 SV=2 ENDD1_HUMAN	945.5543	37	A3	Extracellular	unknown
97	AIYKRVLK	Protein ACN9 homolog, mitochondrial OS=Homo sapiens GN=ACN9 PE=2 SV=1 ACN9_HUMAN	989.6148	25	A3	unknown	unknown
98	KIGDFGLTK	Tyrosine-protein kinase JAK1 OS=Homo sapiens GN=JAK1 PE=1 SV=2 JAK1_HUMAN	977.5706	30	A3	Cytoplasm	Cell communication ; Signal transduction
99	SLMHSFILK*	Dynein light chain roadblock-type 1 OS=Homo sapiens GN=DYNLRB1 PE=1 SV=3 DLRB1_HUMAN	1090,6	45	A3	Cytoplasm	Transport
100	KLLSAEFLE	Calcium-binding protein 39 OS=Homo sapiens GN=CAB39 PE=1 SV=1 CAB39_HUMAN	1048.6005	27	A3	Cytoplasm	unknown
101	KMYEEFLSK	cAMP-dependent protein kinase type I-beta regulatory subunit OS=Homo sapiens GN=PRKAR1B PE=1 SV=4 KAP1_HUMAN	1189,58	36	A3	Cytoplasm	Cell communication ; Signal transduction

102	HVPEHAVVL	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 FAS_HUMAN	999.5768	36	A3	Cytoplasm	Metabolism ; Energy pathways
103	RSDTPLIYK	Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 SYIC_HUMAN	1091.5711	36	A3	Cytoplasm	Protein metabolism
104	EEGPPGPLG	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1 OS=Homo sapiens GN=INPP5D PE=1 SV=2 SHIP1_HUMAN,	851.4351	26	A3	Cytoplasm	Signal transduction ; Cell communication
105	TDKTYAMGH*	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 13B OS=HOMO SAPIENS GN=TNFSF13B PE=1 SV=1TN13B_HUMAN	1038,51	17	A3	Extracellular	Cell communication ; Signal transduction
106	HTFGGPLLK	Zinc finger protein 385A OS=Homo sapiens GN=ZNF385A PE=2 SV=1 Z385A_HUMAN	968,57	34	A3	Nucleolus	Transcription factor activity
107	ATTLPIRNK	Ankyrin repeat domain-containing protein 17 OS=Homo sapiens GN=ANKRD17 PE=1 SV=3 ANR17_HUMAN	1012.6345	30	A3	Nucleus	unknown
108	SVYVYKVLK	Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4 H2B1C_HUMAN	1097.6674	36	A3	Nucleus	DNA binding
109	LIAIQTVGP	Histone-lysine N-methyltransferase SETDB1 OS=Homo sapiens GN=SETDB1 PE=1 SV=1 SETB1_HUMAN	910.5821	29	A3	Nucleus	Transcription regulator activity
110	GTFGGLGSK	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 AHNK_HUMAN	822.4259	29	A3	Nucleus	unknown
111	KDTDISIKP	Reticulon-1 OS=Homo sapiens GN=RTN1 PE=1 SV=1	1015.6404	42	A3	Nucleus	Transcription regulator activity
112	GQYGNPLNK	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens GN=ADAM10 PE=1 SV=1 ADA10_HUMAN	989,51	38	A3	Plasma membrane	Protein metabolism
113	GQYGNPLNK	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens GN=ADAM10 PE=1 SV=1 ADA10_HUMAN	989,51	21	A3	Plasma membrane	Protein metabolism
114	MLGALTEVP	Electrogenic sodium bicarbonate cotransporter 1 OS=Homo sapiens GN=SLC4A4 PE=1 SV=1 S4A4_HUMAN	929.4961	31	A3	Plasma membrane	Transport
115	SVNSTVLVK	Junctional adhesion molecule-like OS=Homo sapiens GN=AMICA1 PE=1 SV=1 JAML1_HUMAN	945,55	40	A3	Plasma membrane	Cell communication ; Signal transduction
116	SVNSTVLVK	Junctional adhesion molecule-like OS=Homo sapiens GN=AMICA1 PE=1 SV=1 JAML1_HUMAN	945,55	27	A3	Plasma membrane	Cell communication ; Signal transduction
117	LVALTAVQS	Potassium voltage-gated channel subfamily KQT member 4 OS=Homo sapiens GN=KCNQ4 PE=1 SV=2 KCNQ4_HUMAN	900.5652	27	A3	Plasma membrane	Cell communication ; Signal transduction
118	KVAPAPAVVK	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2 RL7A_HUMAN	978.6446	27	A3	Cytoplasm	Protein metabolism

119	HNYGPGGNKK	Dynein heavy chain 11, axonemal OS=Homo sapiens GN=DNAH11 PE=1 SV=3 DYH11_HUMAN	1070,5	15	A3	Cytoplasm	Cell growth and/or maintenance
120	LTYEALGLCP	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 NLTP_HUMAN	1078,56	25	A3	Cytoplasm	Transport
121	ALKNPPINTK	Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3 ARPC5_HUMAN	1094,67	28	A3	Cytoskeleton	Cell growth and/or maintenance
122	SLLSSGEVPG	Cytoplasmic dynein 2 heavy chain 1 OS=Homo sapiens GN=DYNC2H1 PE=1 SV=4 DYHC2_HUMAN	944,54	52	A3	Golgi apparatus	Cell growth and/or maintenance
123	AVNAHSNILK	Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=1 SV=1 IMMT_HUMAN	1065,59	27	A3	Mitochondrion	Cell growth and/or maintenance
124	KLIDIVSSQK	Serine/threonine-protein kinase Chk1 OS=Homo sapiens GN=CHEK1 PE=1 SV=2 CHK1_HUMAN	1129,64	69	A3	Nucleus	Cell communication ; Signal transduction
125	KLIDIVSSQK	Serine/threonine-protein kinase Chk1 OS=Homo sapiens GN=CHEK1 PE=1 SV=2 CHK1_HUMAN	1129,67	61	A3	Nucleus	Cell communication ; Signal transduction
126	QLLQSQAQQS	Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3 SEP11_HUMAN	1129,64	26	A3	Perinuclear region	Cell cycle ; Vesicle-mediated transport
127	QIFVKTLTGK	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 RL40_HUMAN	1133.6977	37	A3	Ribosome	Protein metabolism
128	CVFPPQSLQV	Putative phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase TPTE2P1 OS=Homo sapiens GN=TPTE2P1 PE=5 SV=1 TPT2L_HUMAN	1116.6582	24	A3	unknown	unknown
129	VKKPVMVIGTC*	Protein NOV homolog OS=Homo sapiens GN=NOV PE=1 SV=1 NOV_HUMAN	1189.5930	26	A3	Extracellular	Cell communication ; Signal transduction
130	RVFVVGVGMTK*	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 NLTP_HUMAN	1207,71	59	A3	Cytoplasm	Transport
131	RVFVVGVGMTK*	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 NLTP_HUMAN	1207,69	38	A3	Cytoplasm	Transport
132	EDLAVNII	Protein delta homolog 1 OS=Homo sapiens GN=DLK1 PE=1 SV=3 DLK1_HUMAN	885.5126	26	B44	Extracellular	Cell communication ; Signal transduction
133	KEEMLAIM	Calsenilin OS=Homo sapiens GN=KCNIP3 PE=1 SV=1 CSEN_HUMAN	963.4785	31	B44	Cytoplasm	Calcium ion binding
134	LDNVLLDA	Protein kinase C zeta type OS=Homo sapiens GN=PRKCZ PE=1 SV=4 KPCZ_HUMAN	871.4665	40	B44	Cytoplasm	Anti-apoptosis ; Signal transduction ; Negative regulation of enzyme activity ; Inflammatory response
135	PEQHVPVL	PECANEX-LIKE PROTEIN 3 OS=HOMO SAPIENS GN=PCNXL3 PE=1 SV=2PCX3_HUMAN	917,44	13	B44	Membrane	unknown

136	AEGIGTGW	DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 TOP2A_HUMAN	789.3612	30	B44	Nucleus	DNA topoisomerase activity
137	GQRAPERL	Transducin-like enhancer protein 6 OS=Homo sapiens GN=TLE6 PE=2 SV=1 TLE6_HUMAN	925.4485	28	B44	Nucleus	Transcription regulator activity
138	AEIGAIVR	Exocyst complex component 3-like protein 4 OS=Homo sapiens GN=EXOC3L4 PE=2 SV=2 EX3L4_HUMAN	827.4722	33	B44	unknown	unknown
139	HEAEVLKQL	Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3 STMN1_HUMAN	1065,6	64	B44	Cytoplasm	Cell growth and/or maintenance ; Signal transduction
140	QELADTLKK	ANKYRIN REPEAT DOMAIN-CONTAINING PROTEIN 26 OS=HOMO SAPIENS GN=ANKRD26 PE=1 SV=3 ANR26_HUMAN	1044,59	20	B44	centrosome	unknown
141	SEIENVHGF	Disks large homolog 1 OS=Homo sapiens GN=DLG1 PE=1 SV=2 DLG1_HUMAN	1030.4973	29	B44	Centrosome	Cell communication ; Signal transduction
142	VENNLILKM*	3-phosphoinositide-dependent protein kinase 1 OS=Homo sapiens GN=PDPK1 PE=1 SV=1 PDPK1_HUMAN	1088.6074	27	B44	Cytoplasm	Signal transduction ; Cell communication
143	QEDEVMRAY*	Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens GN=ARPC3 PE=1 SV=3 ARPC3_HUMAN	1155.4988	30	B44	Cytoplasm	Cell growth and/or maintenance
144	QEFGVPHQY	Bifunctional protein NCOAT OS=Homo sapiens GN=MGEA5 PE=1 SV=2 NCOAT_HUMAN	1103,51	43	B44	Cytoplasm	Metabolism ; Energy pathways
145	SEDKSIRVW	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2 COPA_HUMAN	1118.5786	30	B44	Cytoplasm	Transport
146	AESEIKLKQ	Coiled-coil domain-containing protein 147 OS=Homo sapiens GN=CCDC147 PE=2 SV=1 CC147_HUMAN	1044.5826	25	B44	Cytoplasm	Cell communication ; Signal transduction
147	QELLMAHDF*	EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2 EHD2_HUMAN	1118.5305	28	B44	Cytoplasm	Cell communication ; Signal transduction
148	EEMDFPQLM	Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1 EIF3D_HUMAN	1170.4797	24	B44	Cytoplasm	Protein metabolism
149	AEQDFISKF	Exocyst complex component 1 OS=Homo sapiens GN=EXOC1 PE=1 SV=4 EXOC1_HUMAN	1083,55	41	B44	Cytoplasm	Transport
150	EEVKLIKKM*	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2 FRIL_HUMAN	1132,66	37	B44	Cytoplasm	Transport
151	AENISRVLY	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 PYGL_HUMAN	1063,58	41	B44	Cytoplasm	Metabolism ; Energy pathways
152	SEVDLTRSF	GMP reductase 2 OS=Homo sapiens GN=GMPR2 PE=1 SV=1 GMPR2_HUMAN	1052.5271	42	B44	Cytoplasm	Metabolism ; Energy pathways

153	AEIEIMKKL*	Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2 PE=1 SV=2 IF2B2_HUMAN	1089.6318	32	B44	Cytoplasm	RNA binding
154	AEGDLVRLL	Neutrophil cytosol factor 4 OS=Homo sapiens GN=NCF4 PE=1 SV=2 NCF4_HUMAN	984,57	57	B44	Cytoplasm	Metabolism ; Energy pathways
155	AEKLITQTF	Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 NUDC_HUMAN	1049,58	39	B44	Cytoplasm	Cell communication ; Signal transduction
156	EEGPDVLRW	Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2 SC23A_HUMAN	1099,54	54	B44	Cytoplasm	Transport
157	TEIEGTQKL	Protein-tyrosine kinase 2-beta OS=Homo sapiens GN=PTK2B PE=1 SV=2 FAK2_HUMAN	1017,55	53	B44	Cytoplasm	Signal transduction ; Cell communication
158	EELEQKYTY	Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2 STAT1_HUMAN	1201.5589	30	B44	Cytoplasm	Transcription factor activity
159	NGHVPFKDM*	STE20-related kinase adapter protein alpha OS=Homo sapiens GN=STRADA PE=1 SV=1 STRAA_HUMAN	1059.4477	29	B44	Cytoplasm	protein metabolism
160	AESLIAKKI	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4 TCPB_HUMAN	971,61	53	B44	Cytoplasm	Protein metabolism
161	EENTNILKF	Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1 TMOD3_HUMAN	1106,58	50	B44	Cytoplasm	Cell growth and/or maintenance
162	AEANVMKTL*	Tyrosine-protein kinase HCK OS=Homo sapiens GN=HCK PE=1 SV=5 HCK_HUMAN	991,52	46	B44	Cytoplasm	Cell communication ; Signal transduction
163	NENDIRVMF*	Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2 ACTN1_HUMAN	1179.6050	22	B44	Cytoplasm	Cell growth and/or maintenance
164	MELDDTLKY*	Iron-responsive element-binding protein 2 OS=Homo sapiens GN=IREB2 PE=1 SV=3 IREB2_HUMAN	1093.6788	24	B44	Cytoplasm	RNA binding
165	EENKLVKKI	Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 SEPT7_HUMAN	1099.6768	39	B44	Cytoskeleton	Cell communication ; Signal transduction
166	EEASLLHQF	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2 SPTB2_HUMAN	1072,53	40	B44	Cytoskeleton	Cell growth and/or maintenance
167	AENPFLTHL	Protein kinase C delta type OS=Homo sapiens GN=PRKCD PE=1 SV=2 KPCD_HUMAN	1040.5383	23	B44	Cytosol	Cell communication ; Signal transduction
168	AELTPHQTF	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3 RPN2_HUMAN	1042,51	57	B44	Endoplasmic reticulum	Protein metabolism
169	AEIEIVKDL	Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens GN=P4HA1 PE=1 SV=2 P4HA1_HUMAN	1028,59	58	B44	Endoplasmic reticulum	Metabolism ; Energy pathways ; Protein metabolism

170	EEAPVLMHY	Prostaglandin G/H synthase 1 OS=Homo sapiens GN=PTGS1 PE=1 SV=2 PGH1_HUMAN	1087,53	65	B44	Endoplasmic reticulum	Metabolism ; Energy pathways
171	EEAPVLMHY*	Prostaglandin G/H synthase 1 OS=Homo sapiens GN=PTGS1 PE=1 SV=2 PGH1_HUMAN	1103,52	36	B44	Endoplasmic reticulum	Metabolism ; Energy pathways
172	SESPIVVVL	Signal peptidase complex catalytic subunit SEC11A OS=Homo sapiens GN=SEC11A PE=1 SV=1 C11A_HUMAN	941.5453	42	B44	Endoplasmic reticulum	Protein metabolism
173	DESQVVTRY	Ubiquitin carboxyl-terminal hydrolase 19 OS=Homo sapiens GN=USP19 PE=1 SV=2 UBP19_HUMAN	1095,53	34	B44	Endoplasmic reticulum	Protein metabolism
174	TEANVVRKF	Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3 QSOX1_HUMAN	1062,59	54	B44	Extracellular	Cell cycle
175	EEIAFLKKL	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4 VIME_HUMAN	1089,65	46	B44	Intermediate filament	Cell growth and/or maintenance
176	EEQNFVQKY	C-type lectin domain family 10 member A OS=Homo sapiens GN=CLEC10A PE=2 SV=1 CLC10_HUMAN	1183.5620	31	B44	Membrane	Immune response
177	QEQEIEQRL	Cytochrome c oxidase subunit 6A1, mitochondrial OS=Homo sapiens GN=COX6A1 PE=1 SV=4 CX6A1_HUMAN	1037.4458	23	B44	Mitochondrion	Metabolism ; Energy pathways
178	SEPDFVAKF	Uncharacterized protein C14orf119 OS=Homo sapiens GN=C14orf119 PE=2 SV=1 CN119_HUMAN	1038.5137	37	B44	Mitochondrion	unknown
179	QEDLRTFSW	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 HNRPM_HUMAN	1142.6015	22	B44	Nucleolus	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism
180	DENSVIKSF	Nucleolar protein 11 OS=Homo sapiens GN=NOL11 PE=1 SV=1 NOL11_HUMAN	1037.5023	36	B44	Nucleolus	Transciption regulation
181	NEAGPPEGY	ACIDIC LEUCINE-RICH NUCLEAR PHOSPHOPROTEIN 32 FAMILY MEMBER E OS=HOMO SAPIENS GN=ANP32E PE=1 SV=1AN32E_HUMAN	932,38	21	B44	Nucleus	unknown
182	DEALIGKKF	Chromodomain-helicase-DNA-binding protein 2 OS=Homo sapiens GN=CHD2 PE=1 SV=2 CHD2_HUMAN	1019.5818	43	B44	Nucleus	DNA binding
183	TENDIRVMF*	CUGBP Elav-like family member 1 OS=Homo sapiens GN=CELF1 PE=1 SV=2 CELF1_HUMAN	1139,54	34	B44	Nucleus	RNA-binding
184	NENDIRVMF*	CUGBP Elav-like family member 2 OS=Homo sapiens GN=CELF2 PE=1 SV=1 CELF2_HUMAN	1152,54	23	B44	Nucleus	RNA-binding
185	NENDIRVMF	CUGBP Elav-like family member 2 OS=Homo sapiens GN=CELF2 PE=1 SV=1 CELF2_HUMAN	1136,53	33	B44	Nucleus	RNA-binding
186	SEINKPNFY	Deoxynucleotidyltransferase terminal-interacting protein 2 OS=Homo sapiens GN=DNTTIP2 PE=1 SV=2	1110.5436	25	B44	Nucleus	DNA binding

187	AEINNIIKI	DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 TOP2A_HUMAN	1026.6039	36	B44	Nucleus	DNA topoisomerase activity
188	SEGPPLTSF	E3 ubiquitin-protein ligase UBR5 OS=Homo sapiens GN=UBR5 PE=1 SV=2 UBR5_HUMAN	933,44	31	B44	Nucleus	Protein metabolism
189	AESIVVHTY	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 XPO2_HUMAN	1017.5154	45	B44	Nucleus	Transport
190	EESDLSRQY	General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4 TF3C1_HUMAN	1125,51	31	B44	Nucleus	Transcription factor activity
191	VEELFERKY	General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2 GTF2I_HUMAN	1211.6308	49	B44	Nucleus	Transcription factor activity
192	AEGDLIEHF	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 ROA0_HUMAN	1029,5	50	B44	Nucleus	RNA binding
193	NENDIITHF	Mediator of RNA polymerase II transcription subunit 23 OS=Homo sapiens GN=MED23 PE=1 SV=2 MED23_HUMAN	1101.5309	32	B44	Nucleus	Transcription regulator activity
194	NETLIVSKF	Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1 MEP50_HUMAN	1049.5584	26	B44	Nucleus	unknown
195	QEAGIKTAF	Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3 PUR6_HUMAN	963,51	38	B44	Nucleus	Metabolism ; Energy pathways
196	AEGPPRLAI	Myeloid leukemia factor 2 OS=Homo sapiens GN=MLF2 PE=1 SV=1 MLF2_HUMAN	922,53	46	B44	Nucleus	unknown
197	DEKPLVLEM*	N-acetyltransferase 14 OS=Homo sapiens GN=NAT14 PE=1 SV=1 NAT14_HUMAN	1088.5279	35	B44	Nucleus	Transcription factor activity
198	AENQTVVKY	Nuclear pore complex protein Nup160 OS=Homo sapiens GN=NUP160 PE=1 SV=3 NU160_HUMAN	1050,55	37	B44	Nucleus	Transport
199	EEAEIIRKY	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 PARP1_HUMAN	1149.6180	48	B44	Nucleus	Protein metabolism
200	PDNPQVKEI	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 PRP8_HUMAN	1038,62	20	B44	Nucleus	RNA binding
201	AEVAAEKSF	Pre-mRNA-splicing factor RBM22 OS=Homo sapiens GN=RBM22 PE=1 SV=1 RBM22_HUMAN	950.4751	29	B44	Nucleus	unknown
202	AEDLVVTKY	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2.1G4 PE=1 SV=3 PA2.1G4_HUMAN	1036,54	38	B44	Nucleus	Transcription regulator activity
203	SENDVIRLI	Serine/threonine-protein kinase 17B OS=Homo sapiens GN=STK17B PE=1 SV=1 ST17B_HUMAN	1057.5828	42	B44	Nucleus	Cell communication ; Signal transduction

204	EEMDLFTKY*	Serine/threonine-protein phosphatase 2A regulatory subunit B" subunit gamma OS=Homo sapiens GN=PPP2R3C PE=1 SV=1 P2R3C_HUMAN	1190,54	35	B44	Nucleus	Cell communication ; Signal transduction
205	SELERPHKV	TRANSCRIPTION ELONGATION FACTOR B POLYPEPTIDE 3 OS=HOMO SAPIENS GN=TCEB3 PE=1 SV=2 ELOA1_HUMAN	1093,59	35	B44	Nucleus	Transcription regulator activity
206	EEAHLNTSF	Transcriptional repressor p66-alpha OS=Homo sapiens GN=GATAD2A PE=1 SV=1 P66A_HUMAN	1171.5809	23	B44	Nucleus	Transcription regulator activity
207	SEVILHHEY	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2 U520_HUMAN	1125.5666	33	B44	Nucleus	Ribonucleoprotein
208	SEDGKIHVW	WD repeat-containing protein 82 OS=Homo sapiens GN=WDR82 PE=1 SV=1 WDR82_HUMAN	1069,54	43	B44	Nucleus	unknown
209	AEAAASAYY	WW domain-binding protein 2 OS=Homo sapiens GN=WBP2 PE=1 SV=1 WBP2_HUMAN	915.3992	32	B44	Nucleus	Cell communication ; Signal transduction
210	AELDPVNSY	Zinc finger protein 516 OS=Homo sapiens GN=ZNF516 PE=1 SV=1 ZN516_HUMAN	1006.4398	30	B44	Nucleus	Transcription regulator activity
211	GEEGSARMW*	Single-stranded DNA-binding protein 2 OS=Homo sapiens GN=SSBP2 PE=1 SV=2 SSBP2_HUMAN	1066.4942	24	B44	Nucleus	Transcription regulator activity
212	QESNVRLKL	Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3 SEP11_HUMAN	1085,63	30	B44	Perinuclear region	Cell cycle ; Vesicle-mediated transport
213	GEVLISRVY	AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=1 SV=2 AP2M1_HUMAN	1034.5553	35	B44	Plasma membrane	Transport
214	NESEPIVVY	Endothelin-converting enzyme 1 OS=Homo sapiens GN=ECE1 PE=1 SV=2 ECE1_HUMAN	1048.4845	28	B44	Plasma membrane	Protein metabolism
215	EIPLILYLF	G-PROTEIN COUPLED RECEPTOR 98 OS=HOMO SAPIENS GN=GPR98 PE=1 SV=2GPR98_HUMAN	1119,58	21	B44	Plasma membrane	Cell communication ; Signal transduction
216	AENNIQPIF	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 ITB2_HUMAN	1044,52	38	B44	Plasma membrane	Cell communication ; Signal transduction
217	KEIDSVKYL	Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens GN=RAC2 PE=1 SV=1 RAC2_HUMAN	1093.6141	25	B44	Plasma membrane	Cell communication ; Signal transduction
218	AETPDIKLF	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 RS5_HUMAN	1032,56	44	B44	Ribosome	Protein metabolism
219	SEAKAFHDY	CUGBP Elav-like family member 2 OS=Homo sapiens GN=CELF2 PE=1 SV=1 CELF2_HUMAN	1152.5316	22	B44	unknown	unknown
220	MESDFEQKL*	MOB kinase activator 1A OS=Homo sapiens GN=MOB1A PE=1 SV=4 MOB1A_HUMAN	1046.4871	20	B44	unknown	unknown

221	AEGVPASAY	Spermatogenesis-associated protein 2-like protein OS=Homo sapiens GN=SPATA2.1L PE=2 SV=1 SPA2.1L_HUMAN	863,4	36	B44	unknown	unknown
222	EENAVDVKQY	Folliculin-interacting protein 1 OS=Homo sapiens GN=FNIP1 PE=1 SV=3 FNIP1_HUMAN	1193,57	47	B44	Cytoplasm	protein metabolism
223	EELLGDGHSY	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4 PSB4_HUMAN	1118.4971	34	B44	Cytoplasm	Protein metabolism
224	KDTPALARLF	E3 UBIQUITIN-PROTEIN LIGASE HUWE1 OS=HOMO SAPIENS GN=HUWE1 PE=1 SV=3 HUWE1_HUMAN	1130,55	16	B44	Nucleus	DNA binding
225	TEFEDIKSGY	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 SET_HUMAN	1187,54	40	B44	Nucleus	MHC class I receptor activity
226	EEILKVEQKY	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 SET_HUMAN	1277,7	53	B44	Nucleus	MHC class I receptor activity
227	EEARPLVEFY	Beta-adrenergic receptor kinase 1 OS=Homo sapiens GN=ADRBK1 PE=1 SV=2 RBK1_HUMAN	1251.6288	32	B44	Cytoplasm	Cell communication ; Signal transduction
228	MEQPIKVTEW*	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 PLAK_HUMAN	1275.6351	31	B44	Cytoplasm	Cell communication ; Signal transduction
229	EEVLIHGVSY	Kelch-like protein 22 OS=Homo sapiens GN=KLHL22 PE=1 SV=2 KLH22_HUMAN	1144.5680	35	B44	Cytoplasm	Cell growth and/or maintenance
230	EEQSHPARLY	Nitrogen permease regulator 2-like protein OS=Homo sapiens GN=NPRL2 PE=1 SV=2 NPRL2_HUMAN	1228.6059	28	B44	Cytoplasm	protein metabolism
231	DEHEGPALYY	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1 PSB2_HUMAN	1192,51	52	B44	Cytoplasm	Protein metabolism
232	EEDPNTHILY	Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2 DIAP1_HUMAN	1141.5140	21	B44	Cytoplasm	Cell growth and/or maintenance
233	RENYDIIKTY	Protein fem-1 homolog B OS=Homo sapiens GN=FEM1B PE=1 SV=1 FEM1B_HUMAN	1313.6724	25	B44	Cytoplasm	Apoptosis
234	EEALILDNKY	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3 SPTN1_HUMAN	1206,63	49	B44	Cytoplasm	Cell growth and/or maintenance
235	AELDRQIKSF	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3 SPTN1_HUMAN	1205.6513	35	B44	Cytoplasm	Cell growth and/or maintenance
236	NEVSKIVQTY	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1 PP2AA_HUMAN	1142.5163	23	B44	Cytoplasm	Cell communication ; Signal transduction
237	EEMGDYIRSY*	Coiled-coil domain-containing protein 93 OS=Homo sapiens GN=CCDC93 PE=1 SV=2 CCD93_HUMAN	1277,55	50	B44	Endosome	Transport
238	QETSFTKEAY	TPT1-like protein OS=Homo sapiens PE=1 SV=2 TPT1L_HUMAN	1202,56	42	B44	Extracellular	unknown

239	AELAHILQEP	MAGUK p55 subfamily member 2 OS=Homo sapiens GN=MPP2 PE=1 SV=3 MPP2_HUMAN	1119.5769	26	B44	Membrane	Cell communication ; Signal transduction
240	SEPDFVAKFY	Uncharacterized protein C14orf119 OS=Homo sapiens GN=C14orf119 PE=2 SV=1 CN119_HUMAN	1201,56	39	B44	Mitochondrion	unknown
241	SEMNTDKQYF*	60S ribosomal export protein NMD3 OS=Homo sapiens GN=NMD3 PE=1 SV=1 NMD3_HUMAN	1277.5383	35	B44	Nucleolus	Transport
242	QELQEINRVY	Annexin A2.1 OS=Homo sapiens GN=ANXA2.1 PE=1 SV=2 ANXA2.1_HUMAN	1290,66	60	B44	Nucleus	Signal transduction ; Cell communication
243	EEMKSGLKDF*	E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2 RBP2_HUMAN	1198.5633	36	B44	Nucleus	Cell communication ; Signal transduction
244	GEDVETSKKW	Endothelial differentiation-related factor 1 OS=Homo sapiens GN=EDF1 PE=1 SV=1 EDF1_HUMAN	1177,58	53	B44	Nucleus	Transcription regulator activity
245	EEVLIPDQKY	F-box/LRR-repeat protein 3 OS=Homo sapiens GN=FBXL3 PE=1 SV=1 FBXL3_HUMAN	1232,64	43	B44	Nucleus	Protein metabolism
246	EEAQPIVTKY	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 HNRL2_HUMAN	1176,59	37	B44	Nucleus	RNA binding
247	NEVVAGIKEY	Mortality factor 4-like protein 1 OS=Homo sapiens GN=MORF4L1 PE=1 SV=2 MO4L1_HUMAN	1120.5728	33	B44	Nucleus	Transcription regulator activity
248	DEIENVAKQF	N-acylneuraminate cytidylyltransferase OS=Homo sapiens GN=CMAS PE=1 SV=2 NEUA_HUMAN	1191.5709	32	B44	Nucleus	Metabolism ; Energy pathways
249	SEEAEIIRKY	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 PARP1_HUMAN	1236,64	56	B44	Nucleus	DNA binding
250	SEFIDSQRVW	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 PRP8_HUMAN	1265,6	32	B44	Nucleus	RNA binding
251	GESSFTYRAY	Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=2 SCAFB_HUMAN	1179.5272	37	B44	Nucleus	unknown
252	MEVEVDGQKF*	Spermatid perinuclear RNA-binding protein OS=Homo sapiens GN=STRBP PE=1 SV=1 STRBP_HUMAN	1196,56	45	B44	Nucleus	RNA binding
253	NEIEDTFRQF	V-type proton ATPase subunit F OS=Homo sapiens GN=ATP6V1F PE=1 SV=2 VATF_HUMAN	1297,61	56	B44	Plasma membrane	Metabolism ; Energy pathways
254	NEDNGIIKAF	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 RL4_HUMAN	1119,57	56	B44	Ribosome	Protein metabolism
255	ASMIFTLNGE	Ryanodine receptor 3 OS=Homo sapiens GN=RYR3 PE=1 SV=3 RYR3_HUMAN	1081.5777	28	B44	Sarcoplasmic reticulum	Transport

256	EEMEAFPEKF*	Proteasome assembly chaperone 4 OS=Homo sapiens GN=PSMG4 PE=2 SV=2 PSMG4_HUMAN	1271.5651	30	B44	unknown	unknown
257	PEALLVGKAS	Putative UPF0607 protein ENSP00000332738 OS=Homo sapiens PE=3 SV=3 YF016_HUMAN	983.5416	27	B44	unknown	unknown
258	VNSLNVSAISI	CD166 ANTIGEN OS=HOMO SAPIENS GN=ALCAM PE=1 SV=2 CD166_HUMAN	1115,61	37	B44	Plasma membrane	Immune response
259	EEQGGVGAFQY	CARBOXYPEPTIDASE Q OS=HOMO SAPIENS GN=CPQ PE=1 SV=1CBPQ_HUMAN	1183,56	12	B44	Endoplasmic reticulum	Protein metabolism
260	AEIVEGENHTY	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 FLNA_HUMAN	1260,57	23	B44	Cytoplasm	Cell growth and/or maintenance
261	SESLFVSNHAY	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2 ALDOA_HUMAN	1252,59	38	B44	Cytoplasm	Metabolism ; Energy pathways
262	EEAQFETKKLY	15 kDa selenoprotein OS=Homo sapiens GN=SEP15 PE=1 SV=3 SEP15_HUMAN	1384.6970	30	B44	Endoplasmic reticulum	Protein folding
263	GETLETLTMAT*	DnaJ homolog subfamily C member 13 OS=Homo sapiens GN=DNAJC13 PE=1 SV=5 DJC13_HUMAN	1181.5795	30	B44	Endosome	unknown
264	QEAVLLHEKLY	Intraflagellar transport protein 74 homolog OS=Homo sapiens GN=IFT74 PE=2 SV=1 IFT74_HUMAN	1341.6573	32	B44	Intracellular vesicle	Cell growth and/or maintenance
265	AEDEGVSQRKF	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 CLIC1_HUMAN	1264,62	50	B44	Nucleus	Transport
266	EEEEEQSRSMS	FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1 SP16H_HUMAN	1339,61	29	B44	Nucleus	Transcription factor activity
267	QEAASLLGKKY	Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2 NASP_HUMAN	1206,67	50	B44	Nucleus	Cell communication ; Signal transduction
268	TEGVEDSYKGA	G-PROTEIN COUPLED RECEPTOR 98 OS=HOMO SAPIENS GN=GPR98 PE=1 SV=2GPR98_HUMAN	1154,57	13	B44	Plasma membrane	Cell communication ; Signal transduction
269	EEVDINGTHTY	Natural killer cell receptor 2B4 OS=Homo sapiens GN=CD244 PE=1 SV=2 CD244_HUMAN	1276.5700	25	B44	Plasma membrane	Immune response
270	AANVCLDPIIY	P2Y purinoceptor 14 OS=Homo sapiens GN=P2RY14 PE=1 SV=1 P2Y14_HUMAN	1190.6269	31	B44	Plasma membrane	Cell communication ; Signal transduction
271	QELDSTDGAKVF	Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=1 SV=1 SRP54_HUMAN	1308,63	35	B44	Cytoplasm	Protein metabolism
272	AEIGEGAYGKVF	Cyclin-dependent kinase 6 OS=Homo sapiens GN=CDK6 PE=1 SV=1 CDK6_HUMAN	1239,63	49	B44	Nucleus	Cell communication ; Signal transduction

273	LPENRISK	Interleukin-1 receptor accessory protein OS=Homo sapiens GN=IL1RAP PE=1 SV=2 IL1AP_HUMAN,	955.6371	25	B56	Plasma membrane	Immune response
274	EPPPPPAYR	Thyroid receptor-interacting protein 6 OS=Homo sapiens GN=TRIP6 PE=1 SV=3 TRIP6_HUMAN	1022.4861	32	B56	Nucleus	Transcription regulator activity
275	EPPPPYLPA	Lysosomal-associated transmembrane protein 4A OS=Homo sapiens GN=LAPTM4A PE=1 SV=1 LAP4A_HUMAN	979.4753	29	B56	Golgi apparatus	Transport
276	ISLENSELF	Cell division cycle-associated protein 2 OS=Homo sapiens GN=CDCA2.1 PE=1 SV=2 CDCA2.1_HUMAN	1050.5387	32	B56	Nucleus	Cell cycle
277	PSAPSAPAA	Heparan sulfate glucosamine 3-O-sulfotransferase 2 OS=Homo sapiens GN=HS3ST2 PE=1 SV=1 HS3S2_HUMAN	767,42	41	B56	Plasma membrane	Metabolism ; Energy pathways
278	YPVIMTNEL*	Olfactory receptor 5H6 OS=Homo sapiens GN=OR5H6 PE=2 SV=2 OR5H6_HUMAN	1094.5437	26	B56	Plasma membrane	Cell communication ; Signal transduction
279	SPSIVIALA	Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B PE=1 SV=1 RAB5B_HUMAN	869.5220	26	B56	Plasma membrane	Cell communication ; Signal transduction
280	NPIELLINDK	Neuronal pentraxin-2 OS=Homo sapiens GN=NPTX2 PE=1 SV=2 NPTX2_HUMAN	1167.5844	26	B56	Extracellular	unknown
281	LSSYISINSD	Protocadherin gamma-A2.1 OS=Homo sapiens GN=PCDHGA2.1 PE=2 SV=1 PCDG2_HUMAN	1097.5647	25	B56	Membrane	Cell adhesion
282	GCVAGVLLQPSG	EPIPLAKIN OS=HOMO SAPIENS GN=EPPK1 PE=1 SV=3 EPIPL_HUMAN	1099,68	35	B56	Cytoplasm	Cell growth and/or maintenance
283	APAFPAAVSSMKK*	PH and SEC7 domain-containing protein 2 OS=Homo sapiens GN=PSD2 PE=2 SV=3 PSD2_HUMAN	1319.6168	28	B56	Membrane	Cell communication ; Signal transduction
284	AYVVLA	Myomesin-3 OS=Homo sapiens GN=MYOM3 PE=2 SV=1MYOM3_HUMAN	634.3695	24	#	Cytoplasm	unknown
285	EEVLLL	Golgi phosphoprotein 3-like OS=Homo sapiens GN=GOLPH3L PE=1 SV=1	714,41	41	#	Golgi apparatus	unknown
286	DYVVFV	Sodium-dependent multivitamin transporter OS=Homo sapiens GN=SLC5A6 PE=2 SV=2 SC5A6_HUMAN	740.3717	31	#	Plasma membrane	Transport
287	DDIIIK	SHC SH2 domain-binding protein 1-like protein OS=Homo sapiens GN=SHCBP1L PE=1 SV=2	715.3699	27	#	unknown	unknown
288	QDALAVV	FYVE, RhoGEF and PH domain-containing protein 6 OS=Homo sapiens GN=FGD6 PE=1 SV=2	714.4298	37	#	Cytoplasm	unknown
289	LGGALGV	Neurexophilin-4 OS=Homo sapiens GN=NXPH4 PE=2 SV=3 NXPH4_HUMAN	585.3444	28	#	Extracellular	Cell communication ; Signal transduction

290	FIIQRNKN	Gamma-tubulin complex component 5 OS=Homo sapiens GN=TUBGCP5 PE=1 SV=1 GCP5_HUMAN	1031,62	46	#	Centrosome	Cell growth and/or maintenance
291	YFDEPVEL	ADP-ribosylation factor GTPase-activating protein 3 OS=Homo sapiens GN=ARFGAP3 PE=1 SV=1 ARFG3_HUMAN,	1010.4556	26	#	Cytoplasm	Protein metabolism
292	QKVLVTVP	Lysine-specific histone demethylase 1B OS=Homo sapiens GN=KDM1B PE=1 SV=3	882.5096	25	#	Nucleus	Transciption regulation
293	KTSNLLLSH	Cyclin-dependent kinase 11A OS=Homo sapiens GN=CDK11A PE=1 SV=4 CD11A_HUMAN	1011.5780	31	#	Cytoplasm	Protein metabolism
294	KTGILKLSQ	Pre-mRNA cleavage complex 2 protein Pcf11 OS=Homo sapiens GN=PCF11 PE=1 SV=3 PCF11_HUMAN	986.6216	26	#	Nucleus	RNA binding
295	ISLAAQKFI	Transcription initiation factor TFIID subunit 10 OS=Homo sapiens GN=TAF10 PE=1 SV=1 TAF10_HUMAN	989.5946	29	#	Nucleus	Transcription regulator activity
296	ENLVSTLML	Uncharacterized protein C20orf26 OS=Homo sapiens GN=C20orf26 PE=2 SV=3 CT026_HUMAN	1018.5030	32	#	unknown	unknown
297	LHSLLEANCS	Histone deacetylase complex subunit SAP25 OS=Homo sapiens GN=SAP25 PE=1 SV=2 SAP25_HUMAN	1085.5672	28	#	Cytoplasm	Transciption regulation
298	LCFVGLADTP	DDB1- and CUL4-associated factor 4-like protein 2 OS=Homo sapiens GN=DCAF4L2 PE=1 SV=1 DC4L2_HUMAN	1034.4589	33	#	unknown	Cell communication ; Signal transduction
299	VCPGTLKAIVDS	Latrophilin-2 OS=Homo sapiens GN=LPHN2 PE=1 SV=2 LPHN2_HUMAN	1201.6064	26	#	Plasma membrane	Cell communication ; Signal transduction
300	LVGLPQTISGDSGGM	TSC22 domain family protein 1 OS=Homo sapiens GN=TSC22D1 PE=1 SV=3 T22D1_HUMAN	1430,76	21	#	Cytoplasm	Cell growth and/or maintenance
301	AEVLVV	CARBOXYPEPTIDASE Q OS=HOMO SAPIENS GN=CPQ PE=1 SV=1CBPQ_HUMAN	628,38	32,6	#	Cytoplasm	Metal Binding

THP1МФ

No.	Peptide sequence	Protein name	Measured Mass[M+H]+	Masco t Score	HLA	Subcellular localisation	Biological function
1	YLGQVTTI	SUMO-activating enzyme subunit 2 OS=Homo sapiens GN=UBA2 PE=1 SV=2 SAE2_HUMAN	893,51	32	A*02:01	Nucleus / Cytoplasm	Protein metabolism
2	ALGTAAAL	Melanophilin OS=Homo sapiens GN=MLPH PE=1 SV=1 MELPH_HUMAN	686,38	50	A*02:01	Endosome	Transport
3	QIGIVAVV	Olfactory receptor 51E2 OS=Homo sapiens GN=OR51E2 PE=2 SV=1 O51E2_HUMAN	797,52	47	A*02:01	membrane	Cell communication ; Signal transduction
4	FLLERRLT	Interferon-related developmental regulator 2 OS=Homo sapiens GN=IFRD2 PE=2 SV=3 IFRD2_HUMAN	1046,66	50	A*02:01	Nucleus	Immune response
5	QLPSDVGL	LEUCINE-RICH REPEAT-CONTAINING PROTEIN 36 OS=HOMO SAPIENS GN=LRRC36 PE=2 SV=2LRC36_HUMAN	827,45	36	A*02:01	Cytoplasm	Protein metabolism
6	PLEVNLAI	Ras-like protein family member 12 OS=Homo sapiens GN=RASL12 PE=1 SV=1 RASLC_HUMAN	867,55	46	A*02:01	unknown	Cell communication ; Signal transduction
7	QVDPEFLG	E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens GN=HERC2 PE=1 SV=2 HERC2_HUMAN	903,45	20	A*02:01	Cytoplasm	Protein metabolism
8	ALLDKLYAL	U3 small nucleolar ribonucleoprotein protein IMP3 OS=Homo sapiens GN=IMP3 PE=1 SV=1 IMP3_HUMAN	1018,64	25	A*02:01	Nucleus	Ribonuclease activity
9	FLDDVVHSL	Probable JmjC domain-containing histone demethylation protein 2C OS=Homo sapiens GN=JMJD1C PE=1 SV=2 JHD2C_HUMAN	1043,56	41	A*02:01	Nucleus	Transcription factor activity/regulator activity
10	FLLGNLSFL	Olfactory receptor 4L1 OS=Homo sapiens GN=OR4L1 PE=2 SV=1 OR4L1_HUMAN	1022,55	20	A*02:01	membrane	Cell communication ; Signal transduction

11	FLYDDNQRV	DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 TOP2A_HUMAN	1168,6	45	A*02:01	Nucleus	other
12	ILMEHIHKL	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1 RL19_HUMAN	1132,68	57	A*02:01	Ribosome	Protein metabolism
13	TLADVLYHV	Set1/Ash2 histone methyltransferase complex subunit ASH2 OS=Homo sapiens GN=ASH2L PE=1 SV=1 ASH2L_HUMAN	1029,57	56	A*02:01	Nucleus	DNA binding
14	SLLDIIEKV	Tuberin OS=Homo sapiens GN=TSC2 PE=1 SV=2 TSC2_HUMAN	1028,64	48	A*02:01	Nucleus	Cell communication ; Signal transduction
15	YLLPAIVHI	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 DDX5_HUMAN	1037,68	42	A*02:01	Nucleus	RNA binding
16	IMLEALERV	Small nuclear ribonucleoprotein G-like protein OS=Homo sapiens PE=3 SV=2 RUXGL_HUMAN	1072,63	35	A*02:01	Nucleus	RNA binding
17	IMLEALERV*	Small nuclear ribonucleoprotein G-like protein OS=Homo sapiens PE=3 SV=2 RUXGL_HUMAN	1088,63	52	A*02:01	Nucleus	RNA binding
18	KLLSVLAQV	MIDASIN OS=HOMO SAPIENS GN=MDN1 PE=1 SV=2MDN1_HUMAN	969,59	32	A*02:01	Nucleus	protein metabolism
19	RMLPHAPGV	Histone deacetylase 2 OS=Homo sapiens GN=HDAC2 PE=1 SV=2 HDAC2_HUMAN	976,56	44	A*02:01	Nucleus	Transcription factor activity/regulator activity
20	SLASLLVSV	Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3 EXOS7_HUMAN	887,57	61	A*02:01	Nucleus	Ribonuclease activity
21	SLLDEFYKL	Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2 CAPR1_HUMAN	1126,63	36	A*02:01	Plasma membrane	Transport
22	YIDDVFHAL	GTP-binding protein Rit1 OS=Homo sapiens GN=RIT1 PE=1 SV=1 RIT1_HUMAN	1091,56	33	A*02:01	Plasma membrane	Cell communication ; Signal transduction

23	KLIEILEQL	DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 12 OS=HOMO SAPIENS GN=DHRS12 PE=2 SV=2 DHR12_HUMAN	1097,76	24	A*02:01	unknown	unknown
24	SMLDDLRNV	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 ITB2_HUMAN	1061,55	54	A*02:01	Plasma membrane	Cell communication ; Signal transduction
25	FLSTLEHHL	Nicalin OS=Homo sapiens GN=NCLN PE=1 SV=2 NCLN_HUMAN	1095,6	38	A*02:01	Plasma membrane	Protein metabolism
26	GLMDTVKKV	Glucocorticoid modulatory element-binding protein 1 OS=Homo sapiens GN=GMEB1 PE=1 SV=2 GMEB1_HUMAN	989,59	56	A*02:01	Nucleus	Transcription factor activity/regulator activity
27	KVIDEIYRV	F-box only protein 28 OS=Homo sapiens GN=FBXO28 PE=1 SV=1 FBX28_HUMAN	1133,67	42	A*02:01	Nucleus / Cytoplasm	Protein metabolism
28	TLYEAVREV	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 RL10A_HUMAN	1078,59	50	A*02:01	Ribosome	Protein metabolism
29	VLIDYQRNV	Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 XPO1_HUMAN	1118,63	52	A*02:01	Nucleus	Cell communication ; Signal transduction
30	TLFDYEVRL	E3 ubiquitin-protein ligase UHRF1 OS=Homo sapiens GN=UHRF1 PE=1 SV=1 UHRF1_HUMAN	1154,64	57	A*02:01	Nucleus	Cell cycle
31	LLSAKLPEL	Uncharacterized protein C20orf194 OS=Homo sapiens GN=C20orf194 PE=1 SV=1 CT194_HUMAN	982,6	47	A*02:01	unknown	unknown
32	TLADIIARL	Protein NYNRIN OS=Homo sapiens GN=NYNRIN PE=1 SV=3 NYNRI_HUMAN	984,62	61	A*02:01	unknown	unknown
33	QLVDIIEKV	Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 PSME3_HUMAN	1055,65	47	A*02:01	Cytoplasm	Protein metabolism
34	ILTDITKGV	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 EF2_HUMAN	958,59	40	A*02:01	Cytoplasm	Protein metabolism

35	SLCPDLMEI	Nucleolar protein 11 OS=Homo sapiens GN=NOL11 PE=1 SV=1 NOL11_HUMAN	1019,5	46	A*02:01	Nucleus	Transcription factor activity/regulator activity
36	TLLDRMVHL	Negative elongation factor C/D OS=Homo sapiens GN=TH1L PE=1 SV=2 NELFD_HUMAN	1096,64	24	A*02:01	Nucleus	Transcription factor activity/regulator activity
37	AIVDKVPSV	Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 COPG1_HUMAN	926,57	59	A*02:01	Golgi apparatus	Transport
38	ALVALTLVA	Arylsulfatase E OS=Homo sapiens GN=ARSE PE=1 SV=2 ARSE_HUMAN	869,55	58	A*02:01	Golgi apparatus	Metabolism ; Energy pathways
39	KVLDFEHFL	MYOSIN LIGHT POLYPEPTIDE 6 OS=HOMO SAPIENS GN=MYL6 PE=1 SV=2 MYL6_HUMAN	1146,66	43	A*02:01	Cytoplasm	Cell growth and/or maintenance
40	SIIGRLLEV	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 PP1A_HUMAN	998,66	31	A*02:01	Cytoskeleton	Cell growth and/or maintenance
41	SLLENLEKI	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C-LIKE 1 OS=HOMO SAPIENS GN=HNRNPCL1 PE=1 SV=1HNRCL_HUMAN	1057,64	43	A*02:01	Nucleus	unknown
42	RLLEQKVEL	Pinin OS=Homo sapiens GN=PNN PE=1 SV=4 PININ_HUMAN	1126,7	44	A*02:01	Plasma membrane	Cell communication ; Signal transduction
43	ILEERSLLV	PROTEIN DISULFIDE-ISOMERASE-LIKE PROTEIN OF THE TESTIS OS=HOMO SAPIENS GN=PDILT PE=1 SV=2PDILT_HUMAN	1070,63	25	A*02:01	Endoplasmic reticulum	Cell growth and/or maintenance
44	MIIVGLSVV	NEURONAL ACETYLCHOLINE RECEPTOR SUBUNIT ALPHA-7 OS=HOMO SAPIENS GN=CHRNA7 PE=1 SV=5 ACHA7_HUMAN	929,6	37	A*02:01	Plasma membrane	Cell communication ; Signal transduction
45	GLLVLYILL	Cytochrome b ascorbate-dependent protein 3 OS=Homo sapiens GN=CYBASC3 PE=1 SV=1 CYAC3_HUMAN	1015,66	50	A*02:01	membrane	Transport
46	VMAPRTLVL*	HLA class I histocompatibility antigen, A-24 alpha chain OS=Homo sapiens GN=A PE=1 SV=2 1A24_HUMAN	1014,62	21	A*02:01	Plasma membrane	Immune response

47	NLSEETNIV	DYNEIN HEAVY CHAIN 10, AXONEMAL OS=HOMO SAPIENS GN=DNAH10 PE=1 SV=4 DYH10_HUMAN	1017,58	27	A*02:01	Cytoskeleton	Cell growth and/or maintenance
48	MITGTLILI*	PROTEIN SPINSTER HOMOLOG 2 OS=HOMO SAPIENS GN=SPNS2 PE=1 SV=2 SPNS2_HUMAN	989,58	40	A*02:01	membrane	Transport
49	ILDQTNVSA	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 HNRPU_HUMAN	959,51	30	A*02:01	Nucleus	RNA binding
50	ALVVQVAEA	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3 HEXB_HUMAN	898,55	78	A*02:01	Lysosome	Metabolism ; Energy pathways
51	ALSNLEVKL	Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1 URP2_HUMAN	985,6	40	A*02:01	Plasma membrane	Cell communication ; Signal transduction
52	AILASLTVI	NIPA-like protein 2 OS=Homo sapiens GN=NIPAL2 PE=2 SV=1 NPAL2_HUMAN	899,58	38	A*02:01	membrane	unknown
53	FVIETARQL	Interferon regulatory factor 2-binding protein 2 OS=Homo sapiens GN=IRF2BP2 PE=1 SV=2 I2BP2_HUMAN	1075,64	46	A*02:01	Nucleus	Transcription factor activity/regulator activity
54	ALLSSLARC	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens GN=MINPP1 PE=1 SV=1 MINP1_HUMAN	932,53	62	A*02:01	Endoplasmic reticulum	Cell communication ; Signal transduction
55	ITLIIMGIV	Tumor suppressor candidate 5 OS=Homo sapiens GN=TUSC5 PE=2 SV=2 TUSC5_HUMAN	971,59	44	A*02:01	membrane	Cell growth and/or maintenance
56	KYTDWTEFL	Scm-like with four MBT domains protein 2 OS=Homo sapiens GN=SFMBT2 PE=1 SV=1 SMBT2_HUMAN	1201,61	44	A*02:01	Nucleus	Transcription factor activity/regulator activity
57	KMRLLNILM*	SWI/SNF-RELATED MATRIX-ASSOCIATED ACTIN-DEPENDENT REGULATOR OF CHROMATIN SUBFAMILY A MEMBER 5 OS=HOMO SAPIENS GN=SMARCA5 PE=1 SV=1SMCA5_HUMAN	1146,66	36	A*02:01	Nucleus	DNA binding
58	KYPENFFLL	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 PP1A_HUMAN	1169,67	27	A*02:01	Cytoskeleton	Cell growth and/or maintenance

59	RYLEQLHQL	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 3 OS=HOMO SAPIENS GN=STAT3 PE=1 SV=2STAT3_HUMAN	1198,68	49	A*02:01	Nucleus	Transcription factor activity/regulator activity
60	IIEPSLRQL	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2 RL40_HUMAN	1067,66	43	A*02:01	Ribosome	Protein metabolism
61	KYPHYFPLL	THIMET OLIGOPEPTIDASE OS=HOMO SAPIENS GN=THOP1 PE=1 SV=2 THOP1_HUMAN	1176,69	29	A*02:01	Cytoplasm	Protein metabolism
62	PVLDIKPYI	NEF-ASSOCIATED PROTEIN 1 OS=HOMO SAPIENS GN=C9ORF156 PE=1 SV=2 NAP1_HUMAN	1056,55	20	A*02:01	unknown	unknown
63	ETLLTAIAV	CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR SUBUNIT 7 OS=HOMO SAPIENS GN=CPSF7 PE=1 SV=1 CPSF7_HUMAN	929,54	26	A*02:01	Nucleus	RNA binding
64	KIMHEIMYK*	SHORT TRANSIENT RECEPTOR POTENTIAL CHANNEL 4-ASSOCIATED PROTEIN OS=HOMO SAPIENS GN=TRPC4AP PE=1 SV=2TP4AP_HUMAN	1207,68	30	A*02:01	Cytoplasm	Cell communication ; Signal transduction
65	LYPQFMFHL	Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2 SC23B_HUMAN	1194,63	31	A*02:01	Endoplasmic reticulum	Transport
66	LYLGLFNRL	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 OS=Homo sapiens GN=SMARCAD1 PE=1 SV=2 SMRCD_HUMAN	1107,69	40	A*02:01	Nucleus	other
67	LSLENLEKI	Phosphatidylinositide phosphatase SAC2 OS=Homo sapiens GN=INPP5F PE=1 SV=3 SAC2_HUMAN	1057,65	51	A*02:01	unknown	unknown
68	TYLEKAIKI	Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens GN=USP7 PE=1 SV=2 UBP7_HUMAN	1077,67	37	A*02:01	Nucleus	Protein metabolism
69	KLDLTLEIQ	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 PRKDC_HUMAN	1071,6	29	A*02:01	Nucleus	Cell communication ; Signal transduction
70	VYSPHVLNL	Dynamin-1 OS=Homo sapiens GN=DNM1 PE=1 SV=2 DYN1_HUMAN	1040,59	33	A*02:01	Mitochondrion	Cell communication ; Signal transduction

71	DLAQIIEAC	Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 EIF3M_HUMAN	974,5	25	A*02:01	Cytoplasm	Protein metabolism
72	IIENIVAVT	RIBOSOMAL L1 DOMAIN-CONTAINING PROTEIN 1 OS=HOMO SAPIENS GN=RSL1D1 PE=1 SV=3RL1D1_HUMAN	970,61	29	A*02:01	Nucleus	Apoptosis
73	LADPENRQL	Beta-1-syntrophin OS=Homo sapiens GN=SNTB1 PE=1 SV=3 SNTB1_HUMAN	1054,55	53	A*02:01	Cytoplasm	Cell communication ; Signal transduction
74	KIYRSMAYE*	Transient receptor potential cation channel subfamily M member 7 OS=Homo sapiens GN=TRPM7 PE=1 SV=1 TRPM7_HUMAN	1175,59	28	A*02:01	Plasma membrane	Transport
75	QIELLKELL	Ryanodine receptor 1 OS=Homo sapiens GN=RYR1 PE=1 SV=3 RYR1_HUMAN	1097,62	26	A*02:01	Sarcoplasmic reticulum	Transport
76	YAIEVDPVL	Cytosolic 5'-nucleotidase 3 OS=Homo sapiens GN=NT5C3 PE=1 SV=3 5NT3_HUMAN	1017,56	50	A*02:01	Cytoplasm	Metabolism ; Energy pathways
77	FVHDLVLYL	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 CLH1_HUMAN	1117,67	52	A*02:01	Cytoplasm	Cell growth and/or maintenance
78	RLLDGAFKL	CLIP-associating protein 1 OS=Homo sapiens GN=CLASP1 PE=1 SV=1 CLAP1_HUMAN	1031,64	45	A*02:01	Centrosome	Cell growth and/or maintenance
79	KLIDDVHRL	Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPR PE=1 SV=2	1107.6400	36	A*02:01	Endoplasmic reticulum	Protein metabolism
80	RLHDVLMEL	Utrophin OS=Homo sapiens GN=UTRN PE=1 SV=2 UTRO_HUMAN	1124,64	29	A*02:01	Cytoplasm	Cell growth and/or maintenance
81	KLLGELHTL	Pericentriolar material 1 protein OS=Homo sapiens GN=PCM1 PE=1 SV=4 PCM1_HUMAN	1022,64	46	A*02:01	Centrosome	Cell growth and/or maintenance
82	SLAEGLRTV	2'-5'-oligoadenylate synthase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=3 OAS3_HUMAN	944,56	56	A*02:01	Cytoplasm	Immune response

83	HLTDITLKV	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 SYK_HUMAN	1038,63	48	A*02:01	Cytoplasm	other
84	GLIEILKKV	Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=1 SV=3 PDCD5_HUMAN	1011,73	57	A*02:01	Cytoplasm	Apoptosis
85	SLLDRFLATV	Cyclin-I OS=Homo sapiens GN=CCNI PE=1 SV=1 CCNI_HUMAN	1133,69	37	A*02:01	unknown	Cell growth and/or maintenance
86	FLWEYGDLHL	Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1 PLD3_HUMAN	1291,68	34	A*02:01	Golgi apparatus	Metabolism ; Energy pathways
87	QLLSALQSLV	Protein DGCR6L OS=Homo sapiens GN=DGCR6L PE=1 SV=2 DGC6L_HUMAN	1070,69	41	A*02:01	Nucleus	unknown
88	KLERVEGAAV	NEF-ASSOCIATED PROTEIN 1 OS=HOMO SAPIENS GN=C9ORF156 PE=1 SV=2 NAP1_HUMAN	1070,69	34	A*02:01	unknown	unknown
89	IVSRITQYIA	Phosphofurin acidic cluster sorting protein 2 OS=Homo sapiens GN=PACS2 PE=1 SV=3 PACS2_HUMAN	1162,64	31	A*02:01	Endoplasmic reticulum	Cell growth and/or maintenance
90	MRYVASYLLA	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1 RLA2_HUMAN	1185,66	51	A*02:01	Cytoplasm	Protein metabolism
91	ALVFAGGIGQ	TRANSMEMBRANE 6 SUPERFAMILY MEMBER 2 OS=HOMO SAPIENS GN=TM6SF2 PE=2 SV=3TM6S2_HUMAN	931,49	27	A*02:01	membrane	Transport
92	KYLIGELVSS	Chromosome-associated kinesin KIF4B OS=Homo sapiens GN=KIF4B PE=1 SV=2 KIF4B_HUMAN	1107,71	42	A*02:01	Nucleus	Cell growth and/or maintenance
93	NIDALKVINK	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4 MACF1_HUMAN	1126,58	22	A*02:01	Cytoplasm	Cell communication ; Signal transduction
94	HLVDEAHCLRL	Proto-oncogene tyrosine-protein kinase ROS OS=Homo sapiens GN=ROS1 PE=1 SV=3 ROS1_HUMAN	1304,73	25	A*02:01	Plasma membrane	Cell communication ; Signal transduction

95	VLFENTDSVHL	RNA-binding protein 34 OS=Homo sapiens GN=RBM34 PE=1 SV=2 RBM34_HUMAN	1272,66	25	A*02:01	Nucleus	RNA binding
96	YILTTGLIPVL	DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 12 OS=HOMO SAPIENS GN=DHRS12 PE=2 SV=2 DHR12_HUMAN	1201,74	26	A*02:01	unknown	unknown
97	MLMPKKNRIAIY	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1 RS10_HUMAN	1476,89	34	A*02:01	Ribosome	Protein metabolism
98	FILLGFFGRWEL	Olfactory receptor 4L1 OS=Homo sapiens GN=OR4L1 PE=2 SV=1 OR4L1_HUMAN	1496,86	25	A*02:01	membrane	Cell communication ; Signal transduction
99	KLLDPEDVAVQL	Utrophin OS=Homo sapiens GN=UTRN PE=1 SV=2 UTRO_HUMAN	1338,78	56	A*02:01	Cytoplasm	Cell growth and/or maintenance
100	RYLDEINLL	Guanine nucleotide-binding protein subunit alpha-15 OS=Homo sapiens GN=GNA15 PE=1 SV=2 GNA15_HUMAN	1147,64	53	A*02:01	Plasma membrane	Cell communication ; Signal transduction
101	MSGEKLVAI*	Protein strawberry notch homolog 2 OS=Homo sapiens GN=SBNO2 PE=2 SV=3 SBNO2_HUMAN	962,58	47	A*02:01	unknown	Metabolism ; Energy pathways
102	VPGAVLVFL	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 DHX9_HUMAN	913,61	21	B*15:11	Nucleus	Transcription factor activity/regulator activity
103	IPAESYTF	26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2 PSMD8_HUMAN	926,46	24	B*15:11	Cytoplasm	Protein metabolism
104	DQLGLMSL	Centrosomal protein of 128 kDa OS=Homo sapiens GN=CEP128 PE=1 SV=2 CE128_HUMAN	875,49	44	B*15:11	Cytoplasm	unknown
105	MDKLVVEY	Abhydrolase domain-containing protein 2 OS=Homo sapiens GN=ABHD2 PE=2 SV=1 ABHD2_HUMAN	995,52	46	B*15:11	membrane	Metabolism ; Energy pathways
106	QPLVAVLI	Contactin-associated protein-like 3B OS=Homo sapiens GN=CNTNAP3B PE=2 SV=2 CNT3B_HUMAN	851,59	46	B*15:11	membrane	Cell communication ; Signal transduction

107	MPYSHPSSY	Nipped-B-like protein OS=Homo sapiens GN=NIPBL PE=1 SV=2 NIPBL_HUMAN	1067,47	46	B*15:11	Nucleus	DNA binding
108	EAASVPVVY	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 FAS_HUMAN	933,52	34	B*15:11	Cytoplasm	Metabolism ; Energy pathways
109	FPYPFQVVY	Tyrosine-protein kinase BTK OS=Homo sapiens GN=BTK PE=1 SV=3 BTK_HUMAN	1158,62	39	B*15:11	Cytoplasm	Cell communication ; Signal transduction
110	MPADTNKAF	ER membrane protein complex subunit 3 OS=Homo sapiens GN=EMC3 PE=1 SV=3 EMC3_HUMAN	993,49	42	B*15:11	membrane	Protein metabolism
111	TAAAVGAVF	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 OS=Homo sapiens GN=NDUFA11 PE=1 SV=3 NDUAB_HUMAN	805,45	46	B*15:11	Mitochondrion	Metabolism ; Energy pathways
112	TPYDSSASY	DNA-binding protein Ikaros OS=Homo sapiens GN=IKZF1 PE=1 SV=1 IKZF1_HUMAN	989,4	41	B*15:11	Nucleus	Transcription factor activity/regulator activity
113	YPKANIVAY	SUMO-activating enzyme subunit 2 OS=Homo sapiens GN=UBA2 PE=1 SV=2 SAE2_HUMAN	1037,57	25	B*15:11	Nucleus / Cytoplasm	Protein metabolism
114	YPNGVCTVY	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3 CAZA2_HUMAN	1014,48	37	B*15:11	Cytoskeleton	Cell growth and/or maintenance
115	YPSPVATSY	Early growth response protein 1 OS=Homo sapiens GN=EGR1 PE=1 SV=1 EGR1_HUMAN	983,51	52	B*15:11	Nucleus	Transcription factor activity/regulator activity
116	IPMTPTSSF	Interferon regulatory factor 2-binding protein 2 OS=Homo sapiens GN=IRF2BP2 PE=1 SV=2 I2BP2_HUMAN	979,51	35	B*15:11	Nucleus	Transcription factor activity/regulator activity
117	LPYNHQHEY	Fatty acid desaturase 2 OS=Homo sapiens GN=FADS2 PE=1 SV=1 FADS2_HUMAN	1199,58	43	B*15:11	Endoplasmic reticulum	Metabolism ; Energy pathways
118	NPVGGLLEY	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 DSRAD_HUMAN	960,53	62	B*15:11	Nucleus	other

119	TPISITSSY	Transducin-like enhancer protein 3 OS=Homo sapiens GN=TLE3 PE=1 SV=2 TLE3_HUMAN	967,52	39	B*15:11	Nucleus	Transcription factor activity/regulator activity
120	YPLEDHTEF	MAP kinase-activating death domain protein OS=Homo sapiens GN=MADD PE=1 SV=2 MADD_HUMAN	1149,53	29	B*15:11	Plasma membrane	other
121	YPNVGKSSF	Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3 NOG1_HUMAN	997,52	37	B*15:11	Nucleus	Cell communication ; Signal transduction
122	YPQVPSSGY	Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3 ANXA7_HUMAN	996,49	44	B*15:11	Nucleus	Transport
123	MPRDDIFVY	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 OS=HOMO SAPIENS GN=USP4 PE=1 SV=3 UBP4_HUMAN	1154,58	41	B*15:11	Nucleus	Protein metabolism
124	DAHPTLVTY	N6-adenosine-methyltransferase 70 kDa subunit OS=Homo sapiens GN=METTL3 PE=1 SV=2 MTA70_HUMAN	1015,53	31	B*15:11	Nucleus	other
125	LPAKILVEF	ZW10 interactor OS=Homo sapiens GN=ZWINT PE=1 SV=2 ZWINT_HUMAN	1028,66	36	B*15:11	Nucleus	Cell cycle
126	MPNGTVQRF	Nucleosome-remodeling factor subunit BPTF OS=Homo sapiens GN=BPTF PE=1 SV=3 BPTF_HUMAN	1048,56	41	B*15:11	Nucleus	Transcription factor activity/regulator activity
127	FPIPGEPGF	Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens GN=ARPC3 PE=1 SV=3 ARPC3_HUMAN	959,52	52	B*15:11	Cytoplasm	Cell growth and/or maintenance
128	HGIDPTGTY	Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 TBB4A_HUMAN	959,48	32	B*15:11	Cytoplasm	Protein metabolism
129	IPYQDRESY	Zinc finger protein 106 homolog OS=Homo sapiens GN=ZFP106 PE=1 SV=1 ZF106_HUMAN	1169,57	39	B*15:11	Nucleus	DNA binding
130	MPYLEHESF	Cell division cycle 7-related protein kinase OS=Homo sapiens GN=CDC7 PE=1 SV=1 CDC7_HUMAN	1151,53	39	B*15:11	Nucleus	Cell communication ; Signal transduction

131	NVIRDAVTY	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 H4_HUMAN	1049,6	45	B*15:11	Nucleus	DNA binding
132	APVPTGEVY	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2 CALX_HUMAN	931,49	36	B*15:11	Endoplasmic reticulum	Protein metabolism
133	SPVDSVLFY	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 CTNB1_HUMAN	1025,54	68	B*15:11	Plasma membrane	Cell communication ; Signal transduction
134	NPADITVLF	Negative elongation factor C/D OS=Homo sapiens GN=TH1L PE=1 SV=2 NELFD_HUMAN	988,55	30	B*15:11	Nucleus	Transcription factor activity/regulator activity
135	YPVDLGDKF	DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Homo sapiens GN=POLR2H PE=1 SV=4 RPAB3_HUMAN	1052,55	53	B*15:11	Nucleus	other
136	MPRDIYQDY	NF-kappa-B-repressing factor OS=Homo sapiens GN=NKRF PE=1 SV=2 NKRF_HUMAN	1199,56	43	B*15:11	Nucleus	Transcription factor activity/regulator activity
137	YPTQPGQGY	RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1 FUS_HUMAN	1009,49	31	B*15:11	Nucleus	other
138	DQMISRIEY	Casein kinase I isoform alpha-like OS=Homo sapiens GN=CSNK1A1L PE=2 SV=2 KC1AL_HUMAN	1153,56	46	B*15:11	Cytoplasm	Cell communication ; Signal transduction
139	LPTGIPIVY	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 PGAM1_HUMAN	971,59	34	B*15:11	Cytoplasm	Metabolism ; Energy pathways
140	NPTLILAAF	Cathepsin L1 OS=Homo sapiens GN=CTSL1 PE=1 SV=2 CATL1_HUMAN	958,58	75	B*15:11	Endosome	Protein metabolism
141	TPVLLSVLY	Sialoadhesin OS=Homo sapiens GN=SIGLEC1 PE=1 SV=2 SN_HUMAN	1003,62	46	B*15:11	Plasma membrane	Immune response
142	GPVGVNVTY	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 FLNA_HUMAN	904,49	39	B*15:11	Cytoplasm	Cell growth and/or maintenance

143	RPAPVEVTY	Protein tyrosine phosphatase type IVA 1 OS=Homo sapiens GN=PTP4A1 PE=1 SV=2 TP4A1_HUMAN	1030,58	46	B*15:11	Nucleus	Cell communication ; Signal transduction
144	DPVGDIVSF	FAS-associated factor 2 OS=Homo sapiens GN=FAF2 PE=1 SV=2 FAF2_HUMAN	947,48	80	B*15:11	Cytoplasm	Apoptosis
145	NAFEVAEKY	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 ACTN4_HUMAN	1069,54	54	B*15:11	Cytoplasm	Cell growth and/or maintenance
146	SPIDVVEKY	Kelch-like protein 12 OS=Homo sapiens GN=KLHL12 PE=1 SV=2 KLH12_HUMAN	1048,56	64	B*15:11	Cytoplasm	Transport
147	TPAEPVQYY	Nuclear transcription factor Y subunit gamma OS=Homo sapiens GN=NFYC PE=1 SV=3 NFYC_HUMAN	1066,54	33	B*15:11	Nucleus	Transcription factor activity/regulator activity
148	GPVLVITEY	Macrophage colony-stimulating factor 1 receptor OS=Homo sapiens GN=CSF1R PE=1 SV=2 CSF1R_HUMAN	989,58	40	B*15:11	Plasma membrane	Cell communication ; Signal transduction
149	IPNEIIHAL	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 HNRPM_HUMAN	1018,62	48	B*15:11	Nucleus	Ribonuclease activity
150	TPVFSKARY	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 RL11_HUMAN	1067,61	35	B*15:11	Ribosome	Protein metabolism
151	VIKQHLTDF	PROTEIN DISULFIDE-ISOMERASE-LIKE PROTEIN OF THE TESTIS OS=HOMO SAPIENS GN=PDILT PE=1 SV=2PDILT_HUMAN	1099,65	28	B*15:11	Endoplasmic reticulum	Cell growth and/or maintenance
152	YWMHVQNTF	Kelch-like protein 24 OS=Homo sapiens GN=KLHL24 PE=2 SV=1 KLH24_HUMAN	1224,58	36	B*15:11	unknown	unknown
153	DPNLEFVAM	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 RAN_HUMAN	1034,51	70	B*15:11	Nucleus	Cell cycle
154	TPEEGGYSY	Microtubule-associated protein 1B OS=Homo sapiens GN=MAP1B PE=1 SV=2 MAP1B_HUMAN	1001,42	31	B*15:11	Cytoplasm	Cell growth and/or maintenance

155	MPDDLLTTL	Cyclic AMP-dependent transcription factor ATF-4 OS=Homo sapiens GN=ATF4 PE=1 SV=3 ATF4_HUMAN	1017,55	61	B*15:11	Nucleus	Transcription factor activity/regulator activity
156	MDNPTTTQY	Dynein light chain roadblock-type 1 OS=Homo sapiens GN=DYNLRB1 PE=1 SV=3 DLRB1_HUMAN	1069,48	30	B*15:11	Cytoplasm	Transport
157	EGRLYQVEY	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1 PSA4_HUMAN	1155,6	40	B*15:11	Cytoplasm	Protein metabolism
158	DPFVDRIGY	Nucleoporin NUP188 homolog OS=Homo sapiens GN=NUP188 PE=1 SV=1 NU188_HUMAN	1080,55	44	B*15:11	Mitochondrion	Transport
159	FPRHIEPEL	Vacuolar fusion protein CCZ1 homolog B OS=Homo sapiens GN=CCZ1B PE=1 SV=1 CCZ1B_HUMAN	1136,62	41	B*15:11	membrane	Transport
160	LPKFEKNFY	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 DDX17_HUMAN	1184,65	32	B*15:11	Nucleus	other
161	DPFKDIILY	Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1 BZW1_HUMAN	1122,63	55	B*15:11	Nucleus	Transcription factor activity/regulator activity
162	EYMKHTRLF	Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2 FLII_HUMAN	1223,64	51	B*15:11	Nucleus	Cell growth and/or maintenance
163	NPDASYVYY	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 SERC_HUMAN	1090,5	28	B*15:11	Cytoplasm	Metabolism ; Energy pathways
164	NPDDVFREF	DnaJ homolog subfamily B member 6 OS=Homo sapiens GN=DNAJB6 PE=1 SV=2 DNJB6_HUMAN	1137,54	44	B*15:11	Cytoplasm	Protein metabolism
165	DPFPAAIIL	Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=3 TOPK_HUMAN	955,57	42	B*15:11	Nucleus	Protein metabolism
166	GSLLPGITY	Receptor-type tyrosine-protein phosphatase F OS=Homo sapiens GN=PTPRF PE=1 SV=2 PTPRF_HUMAN	919,45	34	B*15:11	Plasma membrane	Cell communication ; Signal transduction

167	LPSPREVTV	GON-4-like protein OS=Homo sapiens GN=GON4L PE=1 SV=1 GON4L_HUMAN	996,56	29	B*15:11	Nucleus	DNA binding
168	IWISKLPHF	Tudor domain-containing protein 7 OS=Homo sapiens GN=TDRD7 PE=1 SV=2 TDRD7_HUMAN	1139,68	36	B*15:11	Mitochondrion	Cell communication ; Signal transduction
169	IPISSSNHS	CCR4-NOT transcription complex subunit 4 OS=Homo sapiens GN=CNOT4 PE=1 SV=3 CNOT4_HUMAN	940,54	20	B*15:11	Nucleus	Transcription factor activity/regulator activity
170	KWFFQKLRF	60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2 RL27_HUMAN	1298,79	29	B*15:11	Cytoplasm	Protein metabolism
171	MKDIKSNKF*	LEUCINE-RICH REPEAT-CONTAINING PROTEIN 7 OS=HOMO SAPIENS GN=LRRC7 PE=1 SV=1 LRRC7_HUMAN	1125,57	35	B*15:11	Plasma membrane	Cell growth and/or maintenance
172	VYNSEYYHF	Inactive tyrosine-protein kinase 7 OS=Homo sapiens GN=PTK7 PE=1 SV=2 PTK7_HUMAN	1220,55	44	B*15:11	Plasma membrane	Cell communication ; Signal transduction
173	TYGEIFEKF	NADH dehydrogenase [ubiquinone] 1 subunit C2 OS=Homo sapiens GN=NDUFC2 PE=1 SV=1 NDUC2_HUMAN	1132,6	41	B*15:11	Mitochondrion	Metabolism ; Energy pathways
174	KYSLIKGNF	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1 S10A8_HUMAN	1068,62	50	B*15:11	Cytoplasm	Cell communication ; Signal transduction
175	KYSLIKGNF	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1 S10A8_HUMAN	1068,63	53	B*15:11	Cytoplasm	Cell communication ; Signal transduction
176	MEEILKNEK	Mimitin, mitochondrial OS=Homo sapiens GN=NDUFAF2 PE=1 SV=1 MIMIT_HUMAN	1132,65	51	B*15:11	Mitochondrion	Cell growth and/or maintenance
177	MEEIIKNIQ	Axonemal dynein light chain domain-containing protein 1 OS=Homo sapiens GN=AXDND1 PE=1 SV=1 AXDN1_HUMAN	1116,66	62	B*15:11	unknown	unknown
178	MKDLVKRHH	1-PHOSPHATIDYLINOSITOL 4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA-1 OS=HOMO SAPIENS GN=PLCB1 PE=1 SV=1 PLCB1_HUMAN	1162,72	25	B*15:11	Cytoplasm	Cell communication ; Signal transduction

179	NTIDPSHPM	Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2 SYAC_HUMAN	1010,48	44	B*15:11	Cytoplasm	Protein metabolism
180	VVAPITTGY	Calcyclin-binding protein OS=Homo sapiens GN=CACYBP PE=1 SV=2 CYBP_HUMAN	919,54	32	B*15:11	Cytoplasm	Protein metabolism
181	DLRQELLAF	Phosphatidylinositol 4-kinase beta OS=Homo sapiens GN=PI4KB PE=1 SV=1 PI4KB_HUMAN	1103,64	58	B*15:11	Cytoplasm	Cell communication ; Signal transduction
182	EIDSELEAM*	NESPRIN-1 OS=HOMO SAPIENS GN=SYNE1 PE=1 SV=3SYNE1_HUMAN	1051,54	29	B*15:11	Cytoplasm	Cell growth and/or maintenance
183	YPNSGSVSAY	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2 FLNB_HUMAN	1043,5	44	B*15:11	Cytoplasm	Cell growth and/or maintenance
184	FPMTHGNTGF	Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 PCBP2_HUMAN	1107,53	41	B*15:11	Nucleus	RNA binding
185	FPYDYSASEY	Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2 ACOD_HUMAN	1240,52	34	B*15:11	Endoplasmic reticulum	Metabolism ; Energy pathways
186	FPFIFQGQSY	Matrix metalloproteinase-9 OS=Homo sapiens GN=MMP9 PE=1 SV=3 MMP9_HUMAN	1232,63	38	B*15:11	Extracellular	Protein metabolism
187	FPFIFEGRSY	Matrix metalloproteinase-9 OS=Homo sapiens GN=MMP9 PE=1 SV=3 MMP9_HUMAN	1261,68	52	B*15:11	Extracellular	Protein metabolism
188	MPFEIRLPEF	TATA box-binding protein-like protein 1 OS=Homo sapiens GN=TBPL1 PE=1 SV=1 TBPL1_HUMAN	1277,69	38	B*15:11	Nucleus	Transcription factor activity/regulator activity
189	MPVDPNEPTY	Inhibitor of growth protein 4 OS=Homo sapiens GN=ING4 PE=1 SV=1 ING4_HUMAN	1161,54	33	B*15:11	Nucleus	Transcription factor activity/regulator activity
190	YPFKPPKVTF	Ubiquitin-conjugating enzyme E2 E1 OS=Homo sapiens GN=UBE2E1 PE=1 SV=1 UB2E1_HUMAN	1222,72	39	B*15:11	Nucleus	Protein metabolism

191	SPIPFPPLSY	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 PRP8_HUMAN	1116,62	45	B*15:11	Nucleus	RNA binding
192	LPKSPPYTAF	Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=1 SV=2 IF4B_HUMAN	1119,63	36	B*15:11	Cytoplasm	Protein metabolism
193	LPSPVTAQKY	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 EF2_HUMAN	1102,63	27	B*15:11	Cytoplasm	Protein metabolism
194	LPFPFPSKLY	UPF0464 protein C15orf44 OS=Homo sapiens GN=C15orf44 PE=1 SV=2 CO044_HUMAN	1207,71	33	B*15:11	unknown	unknown
195	HPDEKSIITY	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2 SPTB2_HUMAN	1201,65	44	B*15:11	Cytoskeleton	Cell growth and/or maintenance
196	YGGGGGYDGY	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 ROA3_HUMAN	964,39	29	B*15:11	Nucleus	RNA binding
197	PVLALLLLLY	ATP-binding cassette sub-family A member 1 OS=Homo sapiens GN=ABCA1 PE=1 SV=3 ABCA1_HUMAN	1126,68	30	B*15:11	Plasma membrane	Transport
198	EWDADDFRIF	RNA-binding protein 42 OS=Homo sapiens GN=RBM42 PE=1 SV=1 RBM42_HUMAN	1312,63	39	B*15:11	Nucleus	RNA binding
199	QRKTVQSQIG	PHD finger protein 12 OS=Homo sapiens GN=PHF12 PE=1 SV=2 PHF12_HUMAN	1143,67	22	B*15:11	Nucleus	Transcription factor activity/regulator activity
200	MPAAQEGAVAF	Tapasin OS=Homo sapiens GN=TAPBP PE=1 SV=1 TPSN_HUMAN	1090,54	50	B*15:11	Endoplasmic reticulum	Protein metabolism
201	MPVGPDAILRY	Large proline-rich protein BAG6 OS=Homo sapiens GN=BAG6 PE=1 SV=2 BAG6_HUMAN	1230,69	58	B*15:11	Nucleus	Apoptosis
202	NALPDTLKVTY	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 ITB2_HUMAN	1233,69	41	B*15:11	Plasma membrane	Cell communication ; Signal transduction

203	HPLPETAVRGY	Pre-mRNA-splicing factor SYF1 OS=Homo sapiens GN=XAB2 PE=1 SV=2 SYF1_HUMAN	1238,69	55	B*15:11	Nucleus	DNA binding
204	VPEEGGATHVY	A-kinase-interacting protein 1 OS=Homo sapiens GN=AKIP1 PE=1 SV=2 AKIP1_HUMAN	1157,58	24	B*15:11	Nucleus	Protein metabolism
205	LPKDTSPGSAY	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2 PSMD1_HUMAN	1134,59	41	B*15:11	Cytoplasm	Protein metabolism
206	YPFHDSDPSALF	Tribbles homolog 1 OS=Homo sapiens GN=TRIB1 PE=1 SV=2 TRIB1_HUMAN	1394,66	29	B*15:11	Cytoplasm	Cell communication ; Signal transduction
207	DPLGGSAAIHLY	Macrophage colony-stimulating factor 1 receptor OS=Homo sapiens GN=CSF1R PE=1 SV=2 CSF1R_HUMAN	1212,64	72	B*15:11	Plasma membrane	Cell communication ; Signal transduction
208	GGYGGGGGYDGY	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 ROA3_HUMAN	1078,43	23	B*15:11	Nucleus	RNA binding
209	LGQVAILLFKSG	Dynein light chain 1, cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1 DYL1_HUMAN	1244,79	48	B*15:11	Cytoplasm	Cell growth and/or maintenance
210	HPISSEELLSLKY	Protein C-ets-1 OS=Homo sapiens GN=ETS1 PE=1 SV=1 ETS1_HUMAN	1514,84	42	B*15:11	Nucleus	Transcription factor activity/regulator activity
211	RGVDLDQLLDMSY	40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=1 SV=2 RS15_HUMAN	1523,78	56	B*15:11	Ribosome	other
212	FGKNGSFLPNIQVF	TNF receptor-associated factor 5 OS=Homo sapiens GN=TRAF5 PE=1 SV=2 TRAF5_HUMAN	1566,75	24	B*15:11	Nucleus	Cell communication ; Signal transduction
213	NQWQQGQFWGQKPW	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 HNRPU_HUMAN	1816,94	38	B*15:11	Nucleus	RNA binding
214	GESSGKNVTLPAVF	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 RL4_HUMAN	1404,76	44	B*15:11	Ribosome	Protein metabolism

215	VPDSSGPERIL	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 HNRPK_HUMAN	1168,64	71	B*15:11	Nucleus	Ribonuclease activity
216	FPLPLLKRV	LIPOPOLYSACCHARIDE-BINDING PROTEIN OS=HOMO SAPIENS GN=LBP PE=1 SV=3 LBP_HUMAN	1081,7	47	B*15:11	Extracellular	Immune response
217	SAAAAIVL	CMP-sialic acid transporter OS=Homo sapiens GN=SLC35A1 PE=2 SV=1 S35A1_HUMAN	714,44	43	C*03:03	Golgi apparatus	Transport
218	LAGKIAAL	TRANSMEMBRANE 6 SUPERFAMILY MEMBER 2 OS=HOMO SAPIENS GN=TM6SF2 PE=2 SV=3TM6S2_HUMAN	755,47	31	C*03:03	Endoplasmic reticulum	Metabolism ; Energy pathways
219	IAKDSMTV*	Titin OS=Homo sapiens GN=TTN PE=1 SV=4 TITIN_HUMAN	879,41	28	C*03:03	Nucleus / Cytoplasm	Cell cycle
220	LSQSPMLL	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 PRKDC_HUMAN	887,46	24	C*03:03	Nucleus	Cell communication ; Signal transduction
221	LGSRLMSL	Ryanodine receptor 1 OS=Homo sapiens GN=RYR1 PE=1 SV=3 RYR1_HUMAN	875,49	31	C*03:03	Sarcoplasmic reticulum	Transport
222	SDAIETLL	CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR SUBUNIT 7 OS=HOMO SAPIENS GN=CPSF7 PE=1 SV=1 CPSF7_HUMAN	860,49	27	C*03:03	Nucleus	RNA binding
223	PSAVLQSM	FERM and PDZ domain-containing protein 4 OS=Homo sapiens GN=FRMPD4 PE=1 SV=1 FRPD4_HUMAN	831,41	29	C*03:03	Cytoplasm	Cell communication ; Signal transduction
224	KDAVITVM	OLFACTORY RECEPTOR 1A2 OS=HOMO SAPIENS GN=OR1A2 PE=2 SV=1OR1A2_HUMAN	875,49	41	C*03:03	membrane	Cell communication ; Signal transduction
225	PEQHVPVL	Pecanex-like protein 3 OS=Homo sapiens GN=PCNXL3 PE=1 SV=2 PCX3_HUMAN	917,47	23	C*03:03	membrane	unknown
226	FAVNMFRTL	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform OS=Homo sapiens GN=PPP2R5C PE=1 SV=3 2A5G_HUMAN	1097,62	59	C*03:03	Nucleus	Cell communication ; Signal transduction

227	FAEGQGRAL	Piezo-type mechanosensitive ion channel component 1 OS=Homo sapiens GN=PIEZO1 PE=1 SV=4 PIEZ1_HUMAN	947,51	51	C*03:03	membrane	Transport
228	YAAGVHSVL	AP-5 complex subunit zeta-1 OS=Homo sapiens GN=AP5Z1 PE=1 SV=2 AP5Z1_HUMAN	915,5	33	C*03:03	Cytoplasm	Transport
229	YANSKAVTL	WD repeat-containing protein 82 OS=Homo sapiens GN=WDR82 PE=1 SV=1 WDR82_HUMAN	965,54	38	C*03:03	Nucleus	Cell cycle
230	FAFLTGVGL	Bax inhibitor 1 OS=Homo sapiens GN=TMBIM6 PE=1 SV=2 BI1_HUMAN	923,55	42	C*03:03	membrane	Apoptosis
231	IAISRTPVL	Growth hormone-inducible transmembrane protein OS=Homo sapiens GN=GHITM PE=1 SV=2 GHITM_HUMAN	968,61	46	C*03:03	membrane	unknown
232	TAAPVPTTL	Cell differentiation protein RCD1 homolog OS=Homo sapiens GN=RQCD1 PE=1 SV=1 RCD1_HUMAN	869,51	43	C*03:03	Nucleus	Transcription factor activity/regulator activity
233	TAMDVVYAL	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 H4_HUMAN	981,53	46	C*03:03	Nucleus	DNA binding
234	NAIANASTL	U2 small nuclear ribonucleoprotein A' OS=Homo sapiens GN=SNRPA1 PE=1 SV=2 RU2A_HUMAN	873,47	32	C*03:03	Nucleus	RNA binding
235	SAAFPGASL	DAZ-associated protein 2 OS=Homo sapiens GN=DAZAP2 PE=1 SV=1 DAZP2_HUMAN	819,45	49	C*03:03	Nucleus	RNA binding
236	HAIMRSPQM	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 CTNB1_HUMAN	1069,55	43	C*03:03	Plasma membrane	Cell communication ; Signal transduction
237	AANSVAASL	Interferon alpha-inducible protein 6 OS=Homo sapiens GN=IFI6 PE=2 SV=2 IFI6_HUMAN	802,45	36	C*03:03	Mitochondrion	other
238	MADPNIRFL	Transmembrane protein 173 OS=Homo sapiens GN=TMEM173 PE=1 SV=1 TM173_HUMAN	1075,6	54	C*03:03	membrane	Immune response

239	MADPNIRFL*	Transmembrane protein 173 OS=Homo sapiens GN=TMEM173 PE=1 SV=1 TM173_HUMAN	1091,57	37	C*03:03	membrane	Immune response
240	ISEENFRVM	Kinesin-like protein KIF11 OS=Homo sapiens GN=KIF11 PE=1 SV=2 KIF11_HUMAN	1123,56	47	C*03:03	Cytoplasm	Cell growth and/or maintenance
241	SAACPGLQL	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 ITB2_HUMAN	858,45	29	C*03:03	Plasma membrane	Cell communication ; Signal transduction
242	MSDTTFKAL	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3 CAZA2_HUMAN	1012,52	21	C*03:03	Cytoskeleton	Cell growth and/or maintenance
243	YAVGYMLRL	Chitinase-3-like protein 1 OS=Homo sapiens GN=CHI3L1 PE=1 SV=2 CH3L1_HUMAN	1084,61	49	C*03:03	Extracellular	Cell growth and/or maintenance
244	YYTDIMHTL	Plexin-B2 OS=Homo sapiens GN=PLXNB2 PE=1 SV=3 PLXB2_HUMAN	1155,56	29	C*03:03	Plasma membrane	Cell communication ; Signal transduction
245	KFIDTTSKF	60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 RL3_HUMAN	1085,65	64	C*03:03	Ribosome	Protein metabolism
246	VYIKHPVSL	26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2 PSMD8_HUMAN	1054,65	46	C*03:03	Cytoplasm	Protein metabolism
247	VATPSVHEP	E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens GN=HERC2 PE=1 SV=2 HERC2_HUMAN	935,53	22	C*03:03	Cytoplasm	Protein metabolism
248	IYIKHPHLF	Deoxynucleotidyltransferase terminal-interacting protein 1 OS=Homo sapiens GN=DNTTIP1 PE=1 SV=2 TDIF1_HUMAN	1166,69	31	C*03:03	Nucleus	Immune response
249	LYQDRFDYL	NACHT, LRR and PYD domains-containing protein 3 OS=Homo sapiens GN=NLRP3 PE=1 SV=3 NALP3_HUMAN	1231,62	31	C*03:03	Cytoplasm	Cell communication ; Signal transduction
250	AYVHMVTHF	Bax inhibitor 1 OS=Homo sapiens GN=TMBIM6 PE=1 SV=2 BI1_HUMAN	1103,58	37	C*03:03	membrane	Apoptosis

251	KAQDAGVYQ	Contactin-2 OS=Homo sapiens GN=CNTN2 PE=1 SV=1 CNTN2_HUMAN	978,49	26	C*03:03	Plasma membrane	Cell communication ; Signal transduction
252	TYQDIQNTI	DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens GN=POLR2A PE=1 SV=2 RPB1_HUMAN	1094,56	43	C*03:03	Nucleus	other
253	KYPSPFFVF	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 DHX9_HUMAN	1130,62	27	C*03:03	Nucleus	Transcription factor activity/regulator activity
254	QAELQDEPK	Zinc finger protein 236 OS=Homo sapiens GN=ZNF236 PE=2 SV=2 ZN236_HUMAN	1056,55	48	C*03:03	Nucleus	Transcription factor activity/regulator activity
255	VVATVALTE	Ubiquitin carboxyl-terminal hydrolase 20 OS=Homo sapiens GN=USP20 PE=1 SV=2 UBP20_HUMAN	901,54	23	C*03:03	Endoplasmic reticulum	Protein metabolism
256	VYISEHEHF	Cleft lip and palate transmembrane protein 1 OS=Homo sapiens GN=CLPTM1 PE=1 SV=1 CLPT1_HUMAN	1159,58	46	C*03:03	membrane	Apoptosis
257	KTYGEEMPE*	Dynein heavy chain 17, axonemal OS=Homo sapiens GN=DNAH17 PE=2 SV=2 DYH17_HUMAN	1098,56	31	C*03:03	Extracellular	Metabolism ; Energy pathways
258	PYLFHVVTF	Neurofibromin OS=Homo sapiens GN=NF1 PE=1 SV=2 NF1_HUMAN	1121,64	38	C*03:03	Cytoplasm	Cell communication ; Signal transduction
259	MIMSGFSRLL*	Alkylated DNA repair protein alkB homolog 1 OS=Homo sapiens GN=ALKBH1 PE=1 SV=2 ALKB1_HUMAN	1169,67	41	C*03:03	Nucleus	DNA repair
260	MIMSGFSRLL*	Alkylated DNA repair protein alkB homolog 1 OS=Homo sapiens GN=ALKBH1 PE=1 SV=2 ALKB1_HUMAN	1169,67	23	C*03:03	Nucleus	DNA repair
261	QSISLLLNFL	Dystrobrevin alpha OS=Homo sapiens GN=DTNA PE=1 SV=2 DTNA_HUMAN	1146,66	56	C*03:03	Cytoplasm	Cell communication ; Signal transduction
262	VTGNKILRIL	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2 RS13_HUMAN	1125,74	42	C*03:03	Ribosome	Protein metabolism

263	RSSVLKPLLI	GON-4-like protein OS=Homo sapiens GN=GON4L PE=1 SV=1 GON4L_HUMAN	1124,69	25	C*03:03	Nucleus	DNA binding
264	KYLSVQGQLF	Mitochondrial carrier homolog 1 OS=Homo sapiens GN=MTCH1 PE=1 SV=1 MTCH1_HUMAN	1181,67	50	C*03:03	Mitochondrion	Apoptosis
265	KFIDPIYQVW	RNA polymerase I-specific transcription initiation factor RRN3 OS=Homo sapiens GN=RRN3 PE=1 SV=1 RRN3_HUMAN	1307,75	48	C*03:03	Nucleus	Transcription factor activity/regulator activity
267	RWFQPAIPSW	Protein unc-13 homolog D OS=Homo sapiens GN=UNC13D PE=1 SV=1 UN13D_HUMAN	1286,71	49	C*03:03	Cytoplasm	Transport
268	KYLVIGDLLF	Putative synaptogyrin-2 like protein OS=Homo sapiens PE=5 SV=1 SNG2L_HUMAN	1179,73	36	C*03:03	membrane	unknown
269	FEEDLNNGVT	Dual specificity protein phosphatase 10 OS=Homo sapiens GN=DUSP10 PE=1 SV=1 DUS10_HUMAN	1136,6	47	C*03:03	Cytoplasm	Cell communication ; Signal transduction
270	VDLSTVDKDQ	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3 RPN2_HUMAN	1118,57	22	C*03:03	Endoplasmic reticulum	Protein metabolism
271	GRSPESQMAE	NESPRIN-1 OS=HOMO SAPIENS GN=SYNE1 PE=1 SV=3SYNE1_HUMAN	1090,54	21	C*03:03	Nucleus	Cell growth and/or maintenance
272	YAYDGKDYIAL	HLA class I histocompatibility antigen, A-24 alpha chain OS=Homo sapiens GN=A PE=1 SV=2 1A24_HUMAN	1290,67	24	C*03:03	Plasma membrane	Immune response
273	RSMCTPLPVAA	LEUCINE-RICH REPEAT-CONTAINING PROTEIN 7 OS=HOMO SAPIENS GN=LRRC7 PE=1 SV=1 LRRC7_HUMAN	1144,64	24	C*03:03	Plasma membrane	Cell growth and/or maintenance
274	MRYVASYLL	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1 RLA2_HUMAN	1114,62	40	C*03:03	Cytoplasm	Protein metabolism
275	IYDPNLAFLRF	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2 OS=Homo sapiens GN=PLCG2 PE=1 SV=4 PLCG2_HUMAN	1367,78	58	C*03:03	Cytoplasm	Cell communication ; Signal transduction

276	LHLGYLPNQLF	ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2 DDX1_HUMAN	1313,76	40	C*03:03	Nucleus	RNA binding
277	PATAAASPAAA	Protein SOGA3 OS=Homo sapiens GN=SOGA3 PE=2 SV=1 SOGA3_HUMAN	897,45	37	C*03:03	membrane	unknown
278	GYGGGGGYDGY	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 ROA3_HUMAN	1021,41	42	C*03:03	Nucleus	RNA binding
279	SQVLANGLDNKL	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 RS18_HUMAN	1270,7	54	C*03:03	Ribosome	Protein metabolism
280	DVELDDLGKDEL	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 PDIA6_HUMAN	1359,68	56	C*03:03	Endoplasmic reticulum	Protein metabolism
281	QYIPTELDQVRK	Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1 EIF3M_HUMAN	1488,8	24	C*03:03	Cytoplasm	Protein metabolism
282	TYRGVDLDQLLD	40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=1 SV=2 RS15_HUMAN	1406,75	33	C*03:03	Ribosome	other
283	SDVELDDLGKDEL	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 PDIA6_HUMAN	1446,72	45	C*03:03	Endoplasmic reticulum	Protein metabolism
284	MDVISIDKTGENF	40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 RS4X_HUMAN	1467,73	35	C*03:03	Ribosome	Protein metabolism
285	FAQINQGESITHAL	Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5 CAP1_HUMAN	1527,81	49	C*03:03	Cytoplasm	Cell growth and/or maintenance
286	EITLL	Cyclin-dependent kinase 10 OS=Homo sapiens GN=CDK10 PE=1 SV=1 CDK10_HUMAN	587,33	21	#	unknown	Cell cycle
287	GNFGF	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 RL11_HUMAN	540,25	24	#	Ribosome	Protein metabolism

288	AYVVLA	Myomesin-3 OS=Homo sapiens GN=MYOM3 PE=2 SV=1 MYOM3_HUMAN	634,38	44	#	Cytoplasm	unknown
289	CLVIIY	Uncharacterized protein C4orf32 OS=Homo sapiens GN=C4orf32 PE=1 SV=2 CD032_HUMAN	722,39	36	#	membrane	unknown
290	DEIVAL	Cyclin-dependent kinase 10 OS=Homo sapiens GN=CDK10 PE=1 SV=1 CDK10_HUMAN	658,37	25	#	Plasma membrane	Transport
291	DISLVL	NACHT, LRR and PYD domains-containing protein 3 OS=Homo sapiens GN=NLRP3 PE=1 SV=3 NALP3_HUMAN	658,4	31	#	Cytoplasm	Cell communication ; Signal transduction
292	DLLSVI	Ubiquitin carboxyl-terminal hydrolase 20 OS=Homo sapiens GN=USP20 PE=1 SV=2 UBP20_HUMAN	658,4	27	#	Endoplasmic reticulum	Protein metabolism
293	DVVYAL	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 H4_HUMAN	678,39	36	#	Nucleus	DNA binding
294	EEVLLL	GOLGI PHOSPHOPROTEIN 3-LIKE OS=HOMO SAPIENS GN=GOLPH3L PE=1 SV=1GLP3L_HUMAN	714,43	36	#	Golgi apparatus	Transport
295	FVAATY	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3 RPN2_HUMAN	670,35	22	#	Endoplasmic reticulum	Protein metabolism
296	GLTVVI	Nucleosome-remodeling factor subunit BPTF OS=Homo sapiens GN=BPTF PE=1 SV=3 BPTF_HUMAN	600,36	26	#	Nucleus	Transcription factor activity/regulator activity
297	GNPDPE	Receptor-type tyrosine-protein phosphatase F OS=Homo sapiens GN=PTPRF PE=1 SV=2 PTPRF_HUMAN	627,27	22	#	Plasma membrane	Cell communication ; Signal transduction
298	KVIVVG	MALATE DEHYDROGENASE, CYTOPLASMIC OS=HOMO SAPIENS GN=MDH1 PE=1 SV=4MDHC_HUMAN	613,36	33	#	Cytoplasm	Metabolism ; Energy pathways
299	NAFEEL	DNA REPLICATION LICENSING FACTOR MCM3 OS=HOMO SAPIENS GN=MCM3 PE=1 SV=3MCM3_HUMAN	721,37	34	#	Nucleus	DNA binding

300	NSLEEF	Transmembrane and coiled-coil domains protein 3 OS=Homo sapiens GN=TMCC3 PE=2 SV=3 TMCC3_HUMAN	737,36	34	#	membrane	unknown
301	TLVYAL	E3 ubiquitin-protein ligase RNF170 OS=Homo sapiens GN=RNF170 PE=1 SV=2 RN170_HUMAN	678,39	41	#	Endoplasmic reticulum	Protein metabolism
302	NGTGSSP	EXOSOME COMPLEX COMPONENT RRP46 OS=HOMO SAPIENS GN=EXOSC5 PE=1 SV=1 EXOS5_HUMAN	618,3	18	#	Nucleus	Ribonuclease activity
303	ERVSRAL	MYB/SANT-LIKE DNA-BINDING DOMAIN-CONTAINING PROTEIN 2 OS=HOMO SAPIENS GN=MSANTD2 PE=1 SV=1MSD2_HUMAN	829,48	25	#	unknown	unknown
304	KVIVVGN	MALATE DEHYDROGENASE, CYTOPLASMIC OS=HOMO SAPIENS GN=MDH1 PE=1 SV=4MDHC_HUMAN	727,41	33	#	Cytoplasm	Metabolism ; Energy pathways
305	LLVLDLQ	Transient receptor potential cation channel subfamily M member 7 OS=Homo sapiens GN=TRPM7 PE=1 SV=1 TRPM7_HUMAN	812,43	40	#	Plasma membrane	Transport
306	NVASLVI	TITIN OS=HOMO SAPIENS GN=TTN PE=1 SV=4TITIN_HUMAN	714,44	31	#	Nucleus / Cytoplasm	Cell cycle
307	PALTATL	SOLUTE CARRIER ORGANIC ANION TRANSPORTER FAMILY MEMBER 4A1 OS=HOMO SAPIENS GN=SLCO4A1 PE=1 SV=2SO4A1_HUMAN	685,38	25	#	Plasma membrane	Transport
308	QVLVAVV	E3 ubiquitin-protein ligase RNF170 OS=Homo sapiens GN=RNF170 PE=1 SV=2 RN170_HUMAN	726,48	48	#	Endoplasmic reticulum	Protein metabolism
309	VHMVTHF	Bax inhibitor 1 OS=Homo sapiens GN=TMBIM6 PE=1 SV=2 BI1_HUMAN	869,45	43	#	membrane	Apoptosis
310	NTGIATTI	NUCLEOPORIN P58/P45 OS=HOMO SAPIENS GN=NUPL1 PE=1 SV=1NUPL1_HUMAN	789,43	21	#	Nucleus	Transport
311	LSLNSLLP	Transcription factor E3 OS=Homo sapiens GN=TFE3 PE=1 SV=4 TFE3_HUMAN	855,52	49	#	Nucleus	Transcription factor activity/regulator activity

312	DRAFLIEP	Deubiquitinating protein VCIP135 OS=Homo sapiens GN=VCPIP1 PE=1 SV=2 VCIP1_HUMAN	959,6	43	#	Cytoplasm	Protein metabolism
313	VEKLLVLD	Putative 3-phosphoinositide-dependent protein kinase 2 OS=Homo sapiens GN=PDPK2 PE=5 SV=1 PDPK2_HUMAN	927,55	38	#	Cytoplasm	Protein metabolism
314	QKWVELTD	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4 MACF1_HUMAN	1017,56	20	#	Cytoplasm	Cell communication ; Signal transduction
315	KQDLITCLE	Zinc finger protein 675 OS=Homo sapiens GN=ZNF675 PE=1 SV=3 ZN675_HUMAN	1061,58	38	#	Cytoplasm	Cell communication ; Signal transduction
316	PQPDVFPLF	Protein AATF OS=Homo sapiens GN=AATF PE=1 SV=1 AATF_HUMAN	1058,57	32	#	Nucleus	Apoptosis
317	IKQKLILLQ	CHROMOSOME-ASSOCIATED KINESIN KIF4B OS=HOMO SAPIENS GN=KIF4B PE=1 SV=2 KIF4B_HUMAN	1095,77	36	#	Nucleus	Cell growth and/or maintenance
318	CEWVLVAPAG	Cubilin OS=Homo sapiens GN=CUBN PE=1 SV=5 CUBN_HUMAN	1043,59	37	#	membrane	Metabolism ; Energy pathways
319	RGVDLDQLLD	40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=1 SV=2 RS15_HUMAN	1142,64	38	#	Ribosome	other
320	TEVLKTHGLLV	60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2 RL13A_HUMAN	1208,76	37	#	Ribosome	Protein metabolism
321	PKFEVIEKPQA	ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1 ATP5J_HUMAN	1284,76	62	#	Mitochondrion	Metabolism ; Energy pathways
322	VELDDLGKDEL	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1 PDIA6_HUMAN	1244,65	42	#	Endoplasmic reticulum	Protein metabolism
323	SFLPEKSGYPD	UBIQUITIN-CONJUGATING ENZYME E2 O OS=HOMO SAPIENS GN=UBE2O PE=1 SV=3UBE2O_HUMAN	1238,69	25	#	Cytoplasm	Protein metabolism

324	RRKKKITDVLA	Uncharacterized protein C3orf26 OS=Homo sapiens GN=C3orf26 PE=1 SV=2 CC026_HUMAN	1326,88	32	#	unknown	unknown
325	PNKLVELNKLF	NUCLEAR RECEPTOR COACTIVATOR 7 OS=HOMO SAPIENS GN=NCOA7 PE=1 SV=2 NCOA7_HUMAN	1313,76	40	#	Nucleus	Transcription factor activity/regulator activity
326	LHLGYLPNQLFR	ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2 DDX1_HUMAN	1469,88	41	#	Nucleus	RNA binding
327	RQYAKDIGFIKLD	40S ribosomal protein S29 OS=Homo sapiens GN=RPS29 PE=1 SV=2 RS29_HUMAN	1565,92	72	#	Ribosome	Protein metabolism
328	GFGNDGSNFGGGGSY	Heterogeneous nuclear ribonucleoprotein A1-like 2 OS=Homo sapiens GN=HNRNPA1L2 PE=2 SV=2 RA1L2_HUMAN	1391,59	37	#	Nucleus	Transcription factor activity/regulator activity
329	SGESKTLVLSNLSYS	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 NUCL_HUMAN	1583,86	55	#	Nucleus	RNA binding
330	AYSMSTGAVVTESQTY	E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens GN=HERC2 PE=1 SV=2 HERC2_HUMAN	1693,76	27	#	Cytoplasm	Protein metabolism
331	NGFGNDGSNFGGGGSY	Heterogeneous nuclear ribonucleoprotein A1-like 2 OS=Homo sapiens GN=HNRNPA1L2 PE=2 SV=2 RA1L2_HUMAN	1505,65	26	#	unknown	RNA binding
332	PGDSDIIRSMPEQTGEK	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 RL30_HUMAN	1858,98	108	#	Cytoplasm	Protein metabolism
333	SEKGESSGKNVTLPAVF	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 RL4_HUMAN	1748,97	70	#	Ribosome	Protein metabolism
334	AQTSPQGMPQHPPAPQGQ	Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3 FUBP1_HUMAN	1855,91	24	#	Nucleus	Transcription factor activity/regulator activity
335	GDSRGGGGNFGPGPGSNF	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 ROA2_HUMAN	1635,75	29	#	Nucleus	Transcription factor activity/regulator activity

336	GRVRTKTVKKAARVIIEKY	40S ribosomal protein S17-like OS=Homo sapiens GN=RPS17L PE=3 SV=1 RS17L_HUMAN	2215,46	30	#	Ribosome	Protein metabolism
337	SGGGGYLLSGFTVAMDNLK	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 OS=Homo sapiens GN=TRMT6 PE=1 SV=1 TRM6_HUMAN	1885,99	47	#	Nucleus	other
338	NQSQGYNQWQQGQFWGQKPW	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 HNRPU_HUMAN	2494,23	40	#	Nucleus	RNA binding
339	KGVHSHKKKKIRTSPTFRRPK	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 RL23A_HUMAN	2515,63	36	#	Cytoplasm	RNA binding
340	MFLQYYLNEQGDRVYTLKKFD	H/ACA ribonucleoprotein complex subunit 3 OS=Homo sapiens GN=NOP10 PE=1 SV=1 NOP10_HUMAN	2670,43	39	#	Nucleus	Ribonuclease activity
341	APVKKLVVKGGKKKKQVLKFTLD	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 RL22_HUMAN	2551,69	39	#	Ribosome	Protein metabolism
342	KAPIRPDIVNFVHTNLRKNNRQPY	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 RL4_HUMAN	2889,73	78	#	Ribosome	Protein metabolism
343	KAPIRPDIVNFVHTNLRKNNRQPYAV	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 RL4_HUMAN	3059,82	34	#	Ribosome	Protein metabolism
344	KLTSDDVKEQIYKLAKKGLTPSQIGVIL	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2 RS13_HUMAN	3084,9	63	#	Ribosome	Protein metabolism
345	KAPIRPDIVNFVHTNLRKNNRQPYAVSEL	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 RL4_HUMAN	3389,01	36	#	Ribosome	Protein metabolism
346	APRKGKEKKEEQVISLGPQVAEGENVFGVCHI F	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 RS14_HUMAN	3623,05	96	#	Ribosome	Protein metabolism
347	KSGNFGGSRNMGGPYGGGNYGPGGSGGSGGY GGRSRY	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 ROA2_HUMAN	3485,61	73	#	Nucleus	RNA binding

THP1MΦi

No.	Peptide sequence	Protein name	Measured Mass[M+H]+	Mascot Score	HLA	Subcellular localisation	Biological function
1	SLIMQDDP	Parathyroid hormone 2 receptor OS=Homo sapiens GN=PTH2R PE=1 SV=1 PTH2R_HUMAN	917,4	30	A*02:01	Plasma Membrane	Cell communication ; Signal transduction
2	TLSVPRLP	Plexin-B3 OS=Homo sapiens GN=PLXNB3 PE=1 SV=2 PLXB3_HUMAN	881,58	33	A*02:01	Plasma Membrane	Cell communication ; Signal transduction
3	AVVLGTLHP	EXOSOME COMPLEX COMPONENT RRP46 OS=HOMO SAPIENS GN=EXOSC5 PE=1 SV=1 EXOS5_HUMAN	905,45	22	A*02:01	Nucleolus	Ribonuclease activity
4	KLGNLAKPT	Myelin P2 protein OS=Homo sapiens GN=PMP2 PE=1 SV=3 MYP2_HUMAN	940,55	26	A*02:01	Cytoplasm	Transport
5	TAMDVVYAL	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 H4_HUMAN	981,49	21	A*02:01	Nucleus	DNA binding
6	SMLDDLRNV*	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 ITB2_HUMAN	1077,47	38	A*02:01	Plasma Membrane	Cell communication ; Signal transduction
7	ALSNLEVKL	Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1 URP2_HUMAN	985,53	39	A*02:01	Plasma Membrane	unknown
8	LLGPRLVLA	TransMembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2 TMEDA_HUMAN	950,59	35	A*02:01	Membrane	Transport
9	TLSDLRVYL	Sulfiredoxin-1 OS=Homo sapiens GN=SRXN1 PE=1 SV=2 SRXN1_HUMAN	1078,57	55	A*02:01	Cytoplasm	Stress response
10	VLMTEDIKL*	Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4 IF4G1_HUMAN	1076,55	44	A*02:01	Cytoplasm	Protein metabolism
11	YIMGYISKV*	Unconventional myosin-If OS=Homo sapiens GN=MYO1F PE=1 SV=3 MYO1F_HUMAN	1088,51	38	A*02:01	Cytoplasm	Cell growth and/or maintenance
12	VMAPRTLLL*	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-1 ALPHA CHAIN OS=HOMO SAPIENS GN=A PE=1 SV=1 1A01_HUMAN	1028,57	35	A*02:01	Plasma Membrane	Immune response
13	QTMGAPALKI*	Kinesin-like protein KIF13B OS=Homo sapiens GN=KIF13B PE=1 SV=1 KI13B_HUMAN	1044,61	23	A*02:01	Cytoplasm	Cell growth and/or maintenance
14	VYNENLVHMI*	Pre-mRNA-splicing factor SPF27 OS=Homo sapiens GN=BCAS2 PE=1 SV=1 SPF27_HUMAN	1246,55	44	A*02:01	Nucleus	Cell communication ; Signal transduction

15	FPMEIRQY*	Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2 STAT1_HUMAN	1098,51	41	B*15:11	Cytoplasm	Transcription factor/Transcription factor activity
16	GPQRSVCE	C-TYPE LECTIN DOMAIN FAMILY 4 MEMBER A OS=HOMO SAPIENS GN=CLEC4A PE=1 SV=1 CLC4A_HUMAN	874,29	17	B*15:11	Plasma Membrane	Immune response
17	NAAVVMAV*	AP-3 complex subunit beta-1 OS=Homo sapiens GN=AP3B1 PE=1 SV=3 AP3B1_HUMAN	789,42	25	B*15:11	Plasma Membrane	Protein metabolism
18	DPNLEFVAM*	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 RAN_HUMAN	1050,48	39	B*15:11	Nucleus	Cell communication ; Signal transduction
19	DQMISRIEY*	Casein kinase I isoform alpha OS=Homo sapiens GN=CSNK1A1 PE=1 SV=2 KC1A_HUMAN	1169,54	27	B*15:11	Cytoplasm	Cell cycle
20	FNDPNAKEM*	Zinc finger RNA-binding protein OS=Homo sapiens GN=ZFR PE=1 SV=2 ZFR_HUMAN	1080,46	30	B*15:11	Nucleus	Transcription factor/Transcription factor activity
21	LEGMPQDTY	DNA-binding protein RFX7 OS=Homo sapiens GN=RFX7 PE=1 SV=1 RFX7_HUMAN	1052,6	26	B*15:11	unknown	unknown
22	LPASINTAY	Matrix metalloproteinase-14 OS=Homo sapiens GN=MMP14 PE=1 SV=3 MMP14_HUMAN	948,49	37	B*15:11	Extracellular	Protein metabolism
23	LPREGEQNF	Nck-associated protein 1-like OS=Homo sapiens GN=NCKAP1L PE=1 SV=3 NCKPL_HUMAN	1088,54	17	B*15:11	Plasma Membrane	unknown
24	MPAAGGVLY*	Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Homo sapiens GN=HGS PE=1 SV=1 HGS_HUMAN	893,45	44	B*15:11	Cytoplasm	Cell communication ; Signal transduction
25	MPLEDMNEF*	Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 PE=1 SV=1 RFA2_HUMAN	1156,45	26	B*15:11	Nucleus	DNA binding
26	MPNGTVQRF*	Nucleosome-remodeling factor subunit BPTF OS=Homo sapiens GN=BPTF PE=1 SV=3 BPTF_HUMAN	1064,52	43	B*15:11	Nucleus	Transcription factor/Transcription factor activity
27	NAFKEITTM*	Transcription initiation factor IIB OS=Homo sapiens GN=GTF2B PE=1 SV=1 TF2B_HUMAN	1069,5	34	B*15:11	Nucleus	Transcription factor/Transcription factor activity
28	NPVGGLLEY	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 DSRAD_HUMAN	960,48	37	B*15:11	Nucleus	Deaminase activity
29	SPTDSTPAL	Regulator of cell cycle RGCC OS=Homo sapiens GN=RGCC PE=1 SV=1 RGCC_HUMAN	887,43	29	B*15:11	unknown	unknown

30	SPVDSVLFY	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 CTNB1_HUMAN	1025,53	37	B*15:11	unknown	unknown
31	TPPTDTILY	Killer cell immunoglobulin-like receptor 3DL1 OS=Homo sapiens GN=KIR3DL1 PE=1 SV=1 KI3L1_HUMAN	1019,54	21	B*15:11	Plasma Membrane	Immune response
32	TPTGIKVVM*	Trafficking protein particle complex subunit 1 OS=Homo sapiens GN=TRAPPC1 PE=1 SV=1 TPPC1_HUMAN	960,52	33	B*15:11	Golgi apparatus	Transport
33	AYVHMVTHF*	Bax inhibitor 1 OS=Homo sapiens GN=TMBIM6 PE=1 SV=2 BI1_HUMAN	1119,49	38	B*15:11	Membrane	Apoptosis
34	FPDKPITQY	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4 OST48_HUMAN	1107,54	41	B*15:11	Endoplasmic reticulum	Metabolism ; Energy pathways
35	FPNIPGKSL	Sphingolipid delta(4)-desaturase DES1 OS=Homo sapiens GN=DEGS1 PE=1 SV=1 DEGS1_HUMAN	971,51	51	B*15:11	Endoplasmic reticulum Membrane	Metabolism ; Energy pathways
36	FYMDTSHLF*	Protein PRRC2C OS=Homo sapiens GN=PRRC2C PE=1 SV=4 PRC2C_HUMAN	1175,45	36	B*15:11	Membrane	unknown
37	IYIINVHSM*	DENN domain-containing protein 3 OS=Homo sapiens GN=DENND3 PE=2 SV=2 DEND3_HUMAN	1104,53	39	B*15:11	unknown	unknown
38	KFIDTTSKF	60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2 RL3_HUMAN	1085,32	38	B*15:11	Cytoplasm	Protein metabolism
39	LPDEIYHVY	N-terminal Xaa-Pro-Lys N-methyltransferase 1 OS=Homo sapiens GN=NTMT1 PE=1 SV=3 NTM1A_HUMAN	1147,51	32	B*15:11	Nucleus	Cell cycle
40	LPDTLKVTY	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2 ITB2_HUMAN	1048,56	63	B*15:11	Plasma Membrane	Cell communication ; Signal transduction
41	LPIEAPIRM*	Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1 COX2_HUMAN	1054,55	42	B*15:11	Mitochondrion	Metabolism ; Energy pathways
42	MMNVSKISF*	Sodium-coupled neutral amino acid transporter 2 OS=Homo sapiens GN=SLC38A2 PE=1 SV=2 S38A2_HUMAN	1087,47	58	B*15:11	Plasma Membrane	Transport
43	NAFEVAEKY	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 ACTN4_HUMAN	1069,49	41	B*15:11	Cytoplasm	Cell growth and/or maintenance
44	NVIRDAVTY	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 H4_HUMAN	1049,3	33	B*15:11	Nucleus	DNA binding

45	SPVDSVLFY	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 CTNB1_HUMAN	1025,46	35	B*15:11	Plasma Membrane	Cell communication ; Signal transduction
46	TYGEIFEKF	NADH dehydrogenase [ubiquinone] 1 subunit C2 OS=Homo sapiens GN=NDUFC2 PE=1 SV=1 NDUC2_HUMAN	1132,51	44	B*15:11	Mitochondrion	Metabolism ; Energy pathways
47	VPLDERIVF	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 NIBL1_HUMAN	1086,57	36	B*15:11	Nucleus	unknown
48	VYAQVARLF	Paired amphipathic helix protein Sin3a OS=Homo sapiens GN=SIN3A PE=1 SV=2 SIN3A_HUMAN	1065,57	41	B*15:11	Nucleus	Transcription factor/Transcription factor activity
49	YPVIMTNEL*	Olfactory receptor 5H6 OS=Homo sapiens GN=OR5H6 PE=2 SV=2 OR5H6_HUMAN	1094,49	31	B*15:11	Plasma Membrane	Cell communication ; Signal transduction
50	FPMTHGNTGF*	Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1 PCBP2_HUMAN	1123,47	30	B*15:11	Nucleus	RNA binding
51	GPPGQQGTPG	Collagen alpha-2(XI) chain OS=Homo sapiens GN=COL11A2 PE=1 SV=5 COBA2_HUMAN	894,52	16	B*15:11	Extracellular	Cell growth and/or maintenance
52	HPMNDPTRTF*	Lysosomal protein NCU-G1 OS=Homo sapiens GN=C1orf85 PE=1 SV=1 NCUG1_HUMAN	1230,6	15	B*15:11	Membrane	unknown
53	LPSPVTAQKY	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 EF2_HUMAN	1102,58	48	B*15:11	Cytoplasm	Protein metabolism
54	MIMQQGMASS*	Mastermind-like domain-containing protein 1 OS=Homo sapiens GN=MAMLD1 PE=1 SV=2 MAMD1_HUMAN	1098,53	16	B*15:11	unknown	unknown
55	ATPVSPAMSY	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2 ITIH3_HUMAN	1022,57	38	B*15:11	Extracellular	Protein metabolism
56	FYMDTSHLF*	Protein PRRC2C OS=Homo sapiens GN=PRRC2C PE=1 SV=4 PRC2C_HUMAN	1176,5	36	B*15:11	RNA binding	Membrane
57	FPASFPNRQY	Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1 HM13_HUMAN	1225,55	41	B*15:11	Membrane	Immune response
58	MPVGPDAILRY*	Large proline-rich protein BAG6 OS=Homo sapiens GN=BAG6 PE=1 SV=2 BAG6_HUMAN	1246,59	77	B*15:11	Cytoplasm	Apoptosis
59	NPILSMLTNQTG*	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2 OS=Homo sapiens GN=B3GNT2 PE=1 SV=2 B3GN2_HUMAN	1303,75	14	B*15:11	Membrane	Metabolism ; Energy pathways

60	YPQQSPYPATGG	Vacuolar protein sorting-associated protein 37C OS=Homo sapiens GN=VPS37C PE=1 SV=2 VP37C_HUMAN	1264,79	19	B*15:11	Endosome	Transport
61	SNEDAADD	Sodium-dependent neutral amino acid transporter B(0)AT2 OS=Homo sapiens GN=SLC6A15 PE=1 SV=1 S6A15_HUMAN	835,36	19	C*03:03	Plasma Membrane	Transport
62	EPPPPPAYR	Thyroid receptor-interacting protein 6 OS=Homo sapiens GN=TRIP6 PE=1 SV=3 TRIP6_HUMAN	1022,51	27	B*15:11	Nucleus	Transcription factor/Transcription factor activity
63	LGVAEALHP	Serine/threonine-protein kinase STK11 OS=Homo sapiens GN=STK11 PE=1 SV=1 STK11_HUMAN	905,45	44	C*03:03	Cytoplasm	Cell communication ; Signal transduction
64	SAAMPGASL*	Beta-1,4-galactosyltransferase 1 OS=Homo sapiens GN=B4GALT1 PE=1 SV=5 B4GT1_HUMAN	819,38	32	C*03:03	Golgi apparatus	Metabolism ; Energy pathways
65	VTVPPGPSL	Putative PIP5K1A and PSMD4-like protein OS=Homo sapiens GN=PIPSL PE=5 SV=1 PIPSL_HUMAN	865,49	27	C*03:03	unknown	unknown
66	YGYTRVAEM*	Matrix metalloproteinase-9 OS=Homo sapiens GN=MMP9 PE=1 SV=3 MMP9_HUMAN	1104,49	46	C*03:03	Extracellular	Protein metabolism
67	EDAELFMAL	Dedicator of cytokinesis protein 5 OS=Homo sapiens GN=DOCK5 PE=1 SV=3 DOCK5_HUMAN	1053,49	40	C*03:03	unknown	Cell communication ; Signal transduction
68	FAEGFVRAL	Transcription factor AP-1 OS=Homo sapiens GN=JUN PE=1 SV=2 JUN_HUMAN	1008,51	55	C*03:03	Nucleus	Transcription factor/Transcription factor activity
69	FVIETARQL	Interferon regulatory factor 2-binding protein-like OS=Homo sapiens GN=IRF2BPL PE=1 SV=1 I2BPL_HUMAN	1075,57	39	C*03:03	Nucleus	Transcription factor/Transcription factor activity
70	SAAFPGASL	DAZ-associated protein 2 OS=Homo sapiens GN=DAZAP2 PE=1 SV=1 DAZP2_HUMAN	819,4	39	C*03:03	unknown	RNA binding
71	MRHTNYSFSP*	Macrophage colony-stimulating factor 1 receptor OS=Homo sapiens GN=CSF1R PE=1 SV=2 CSF1R_HUMAN	1254,5	27	C*03:03	Plasma Membrane	Immune response
72	YVHDAPVRSL	Interleukin-1 beta OS=Homo sapiens GN=IL1B PE=1 SV=2 IL1B_HUMAN	1155,56	42	C*03:03	Extracellular	Immune response
73	TALQQARELQA	TETRATRICOPEPTIDE REPEAT PROTEIN 21B OS=HOMO SAPIENS GN=TTC21B PE=1 SV=2 TT21B_HUMAN	1227,67	11	C*03:03	unknown	unknown

74	YASGRTTGIVM*	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 ACTBL_HUMAN	1170,58	32	C*03:03	unknown	unknown
75	GAVLSPSEKSYQ	Interleukin-1 receptor-associated kinase 3 OS=Homo sapiens GN=IRAK3 PE=1 SV=2 IRAK3_HUMAN	1264,78	19	C*03:03	unknown	Cell communication ; Signal transduction
76	NGADGPQGPPGG	Collagen alpha-2(XI) chain OS=Homo sapiens GN=COL11A2 PE=1 SV=5 COBA2_HUMAN	1022,57	17	C*03:03	Extracellular	Cell growth and/or maintenance
77	PGAAKPALAPSFG	Nuclear envelope pore Membrane protein POM 121 OS=Homo sapiens GN=POM121 PE=1 SV=2 P121A_HUMAN	1182,45	30	C*03:03	Nucleus	Transport
78	IILIL	TETRASPANIN-15 OS=HOMO SAPIENS GN=TSPAN15 PE=2 SV=1 TSN15_HUMAN	583,44	23	#	Membrane	Cell communication ; Signal transduction
79	AHLLLL	PROTOCADHERIN GAMMA-A11 OS=HOMO SAPIENS GN=PCDHGA11 PE=1 SV=1 PCDGB_HUMAN	678,5	42	#	Plasma Membrane	Cell growth and/or maintenance
80	TPRAGE	CTD SMALL PHOSPHATASE-LIKE PROTEIN 2 OS=HOMO SAPIENS GN=CTDSPL2 PE=1 SV=2 CTSL2_HUMAN	629,41	24	#	Nucleus	unknown
81	VPKAVM*	Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2 DNM1L_HUMAN	659,35	20	#	Cytoplasm	Mitochondrion organization and biogenesis
82	DAGVPGH	Laminin subunit alpha-2 OS=Homo sapiens GN=LAMA2 PE=1 SV=4 LAMA2_HUMAN	651,39	31	#	Extracellular	Cell growth and/or maintenance
83	GIPMVLI*	Rho-related GTP-binding protein RhoF OS=Homo sapiens GN=RHOF PE=2 SV=1 RHOF_HUMAN	757,4	28	#	Plasma Membrane	Cell communication ; Signal transduction
84	PGGAGAS	Neuropeptide B OS=Homo sapiens GN=NPB PE=1 SV=1 NPB_HUMAN	515,3	10	#	unknown	Cell communication ; Signal transduction
85	QSGPEEI	Adenylate cyclase type 8 OS=Homo sapiens GN=ADCY8 PE=1 SV=1 ADCY8_HUMAN	758,4	30	#	Plasma Membrane	Cell communication ; Signal transduction
86	ARSQVVF	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2 PLOD1_HUMAN	805,4	39	#	Endoplasmic reticulum	Metabolism ; Energy pathways
87	TYMLSITG*	Olfactory receptor 6C74 OS=Homo sapiens GN=OR6C74 PE=2 SV=1 O6C74_HUMAN	900,32	21	#	Membrane	Cell communication ; Signal transduction

*amino acid methionine oxidized
HLA assignment is undefined

6.2 List of Publications

1. Nyambura, L.W., Jarmalavicius, S., Baleeiro, R.B., Walden, P., 2016. Diverse HLA-I Peptide Repertoires of the APC Lines MUTZ3-Derived Immature and Mature Dendritic Cells and THP1-Derived Macrophages. *The Journal of Immunology 197, 2102.* (doi: 10.4049/jimmunol.1600762)
   (Contribution ≥ 90%)

2. Nyambura, L.W., Jarmalavicius, S., Walden, P. Impact of *Leishmania donovani* Infection on HLA I Peptide Repertoire of the Antigen-Presenting Cell Line THP1-Derived Macrophages *(submitted in PLOS ONE Manuscript No. PONE-D-18-07151)*
   (Contribution ≥ 90%)

3. Baleeiro, R.B., Nyambura, L.W., Jarmalavicius, S., Walden, P. Clearance and processing of leishmania parasites by infected human dendritic cells with efficient induction of T cell responses (submitted)
   (Contribution =20%)

Hiermit erkläre ich, dass ich die vorliegende Arbeit selbstständig und nur mit den angegebenen Hilfsmitteln erstellt habe.

Berlin, Dezember 2017 Lydon Wainaina Nyambura